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FIG. 1A

HEME BIOSYNTHESIS

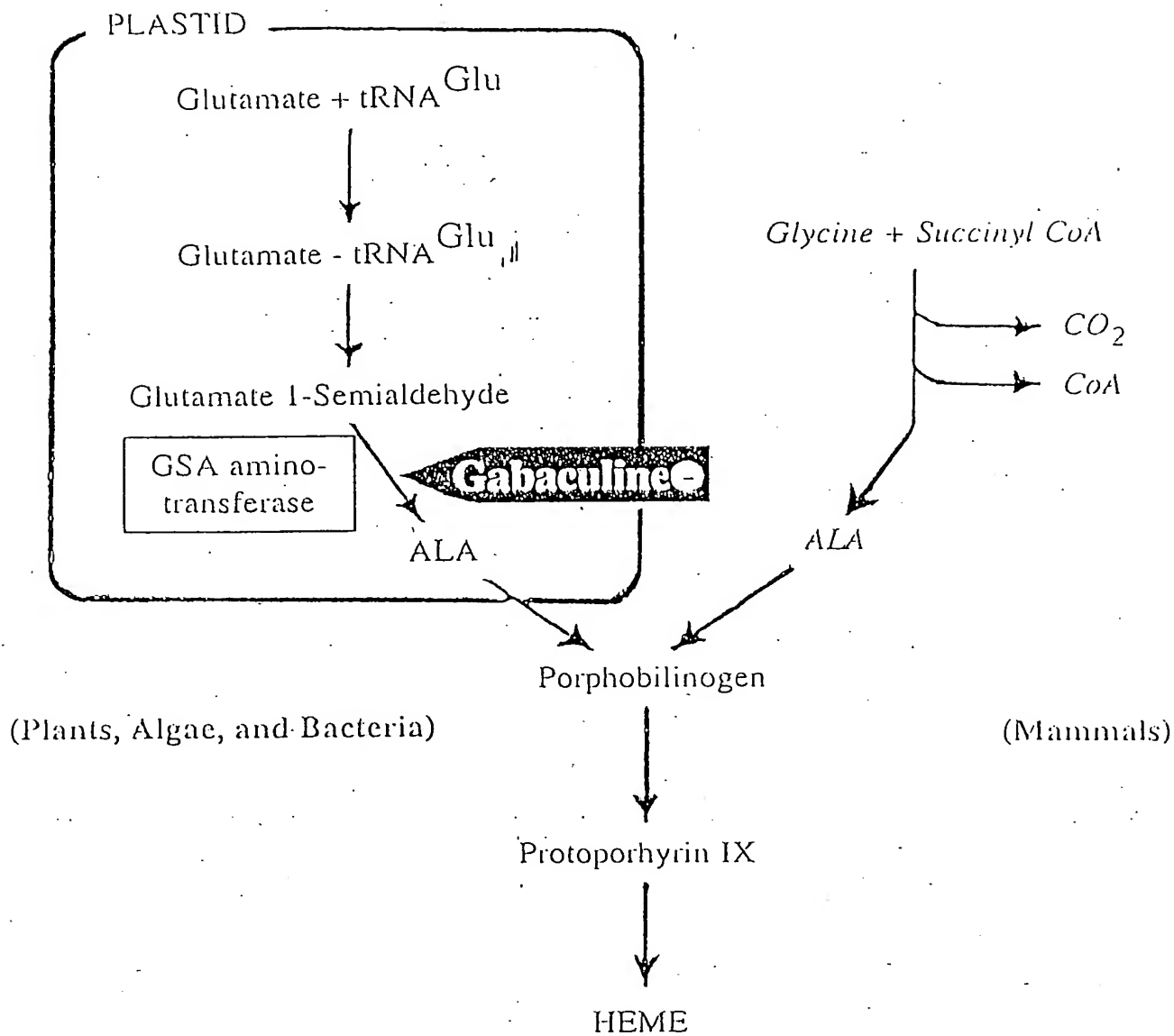


FIG. 1B

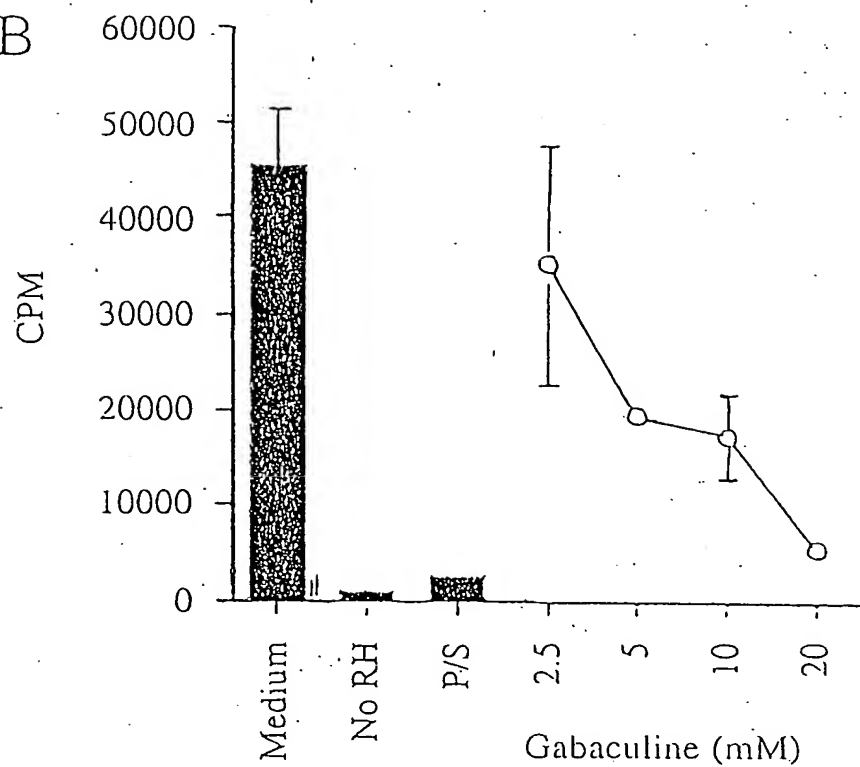


FIG. 1C

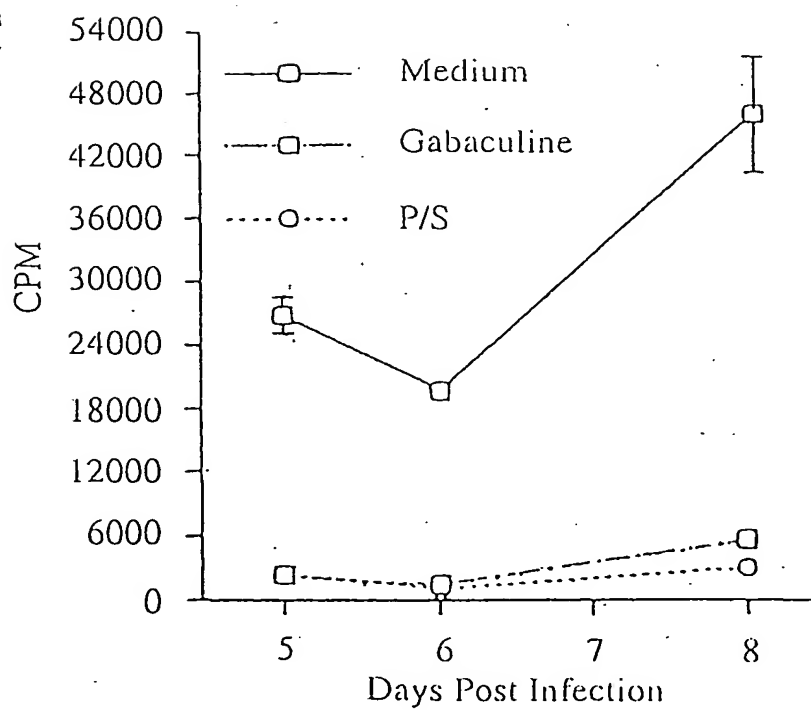


FIG. 2A

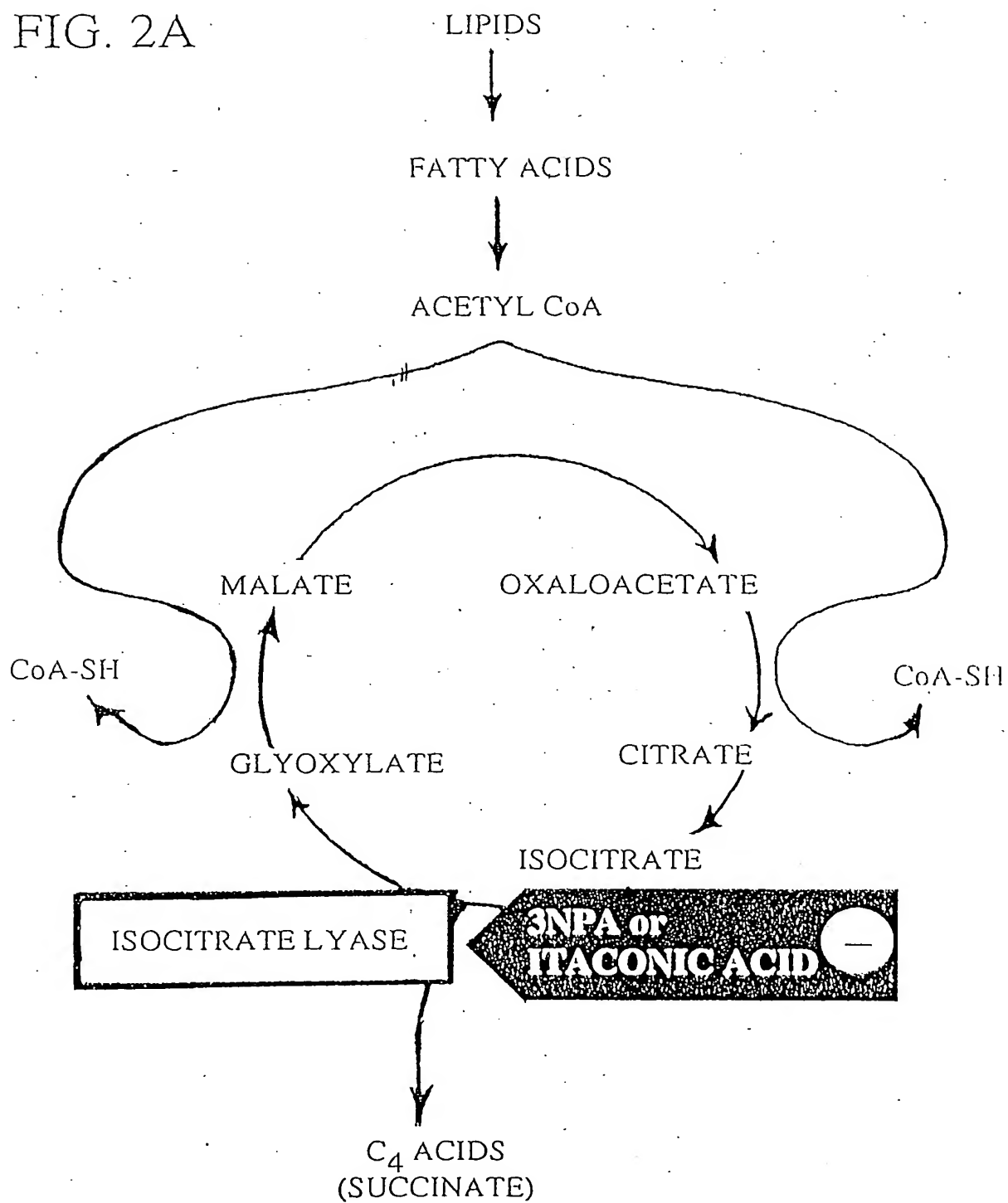


FIG. 2B

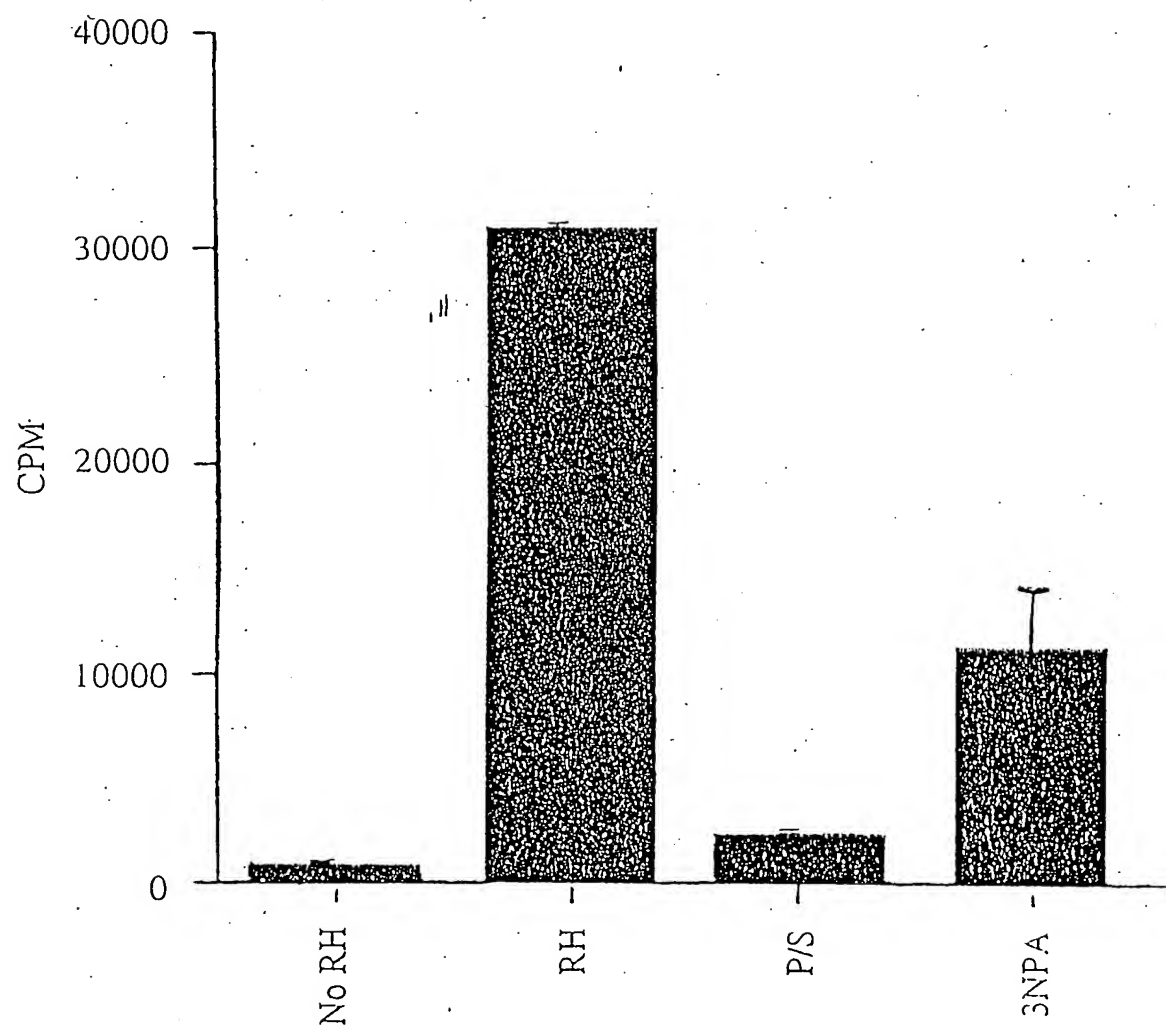


FIG. 3A

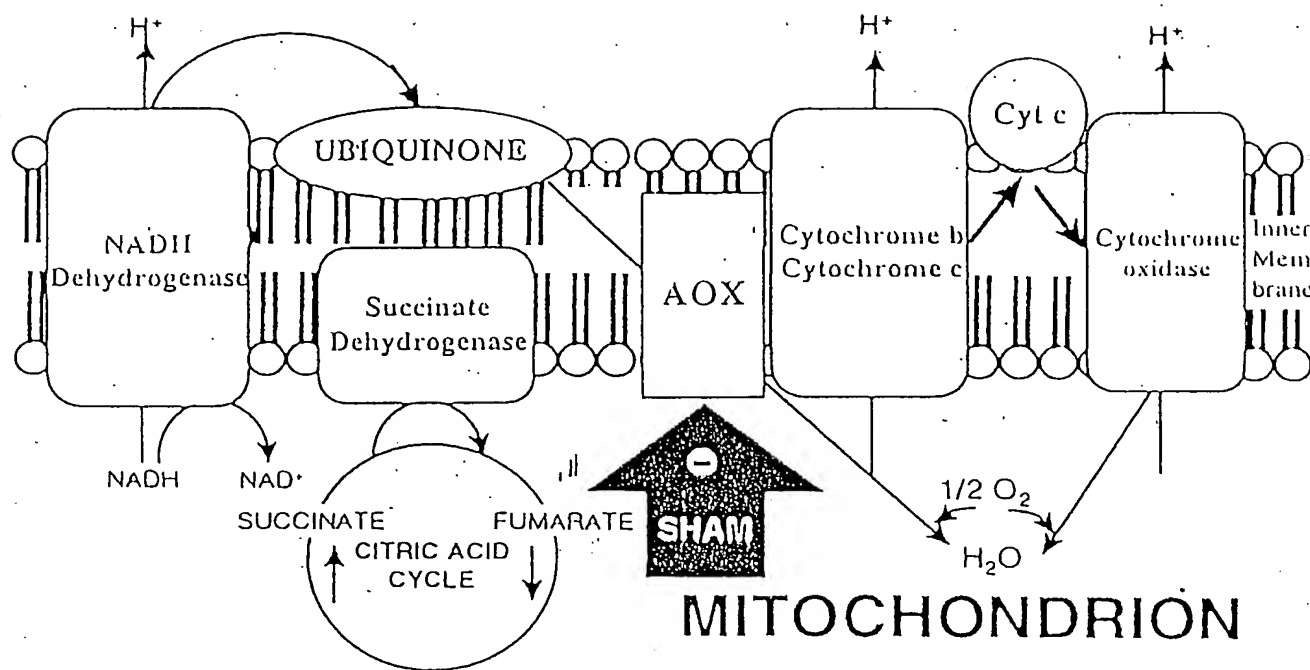


FIG. 3B

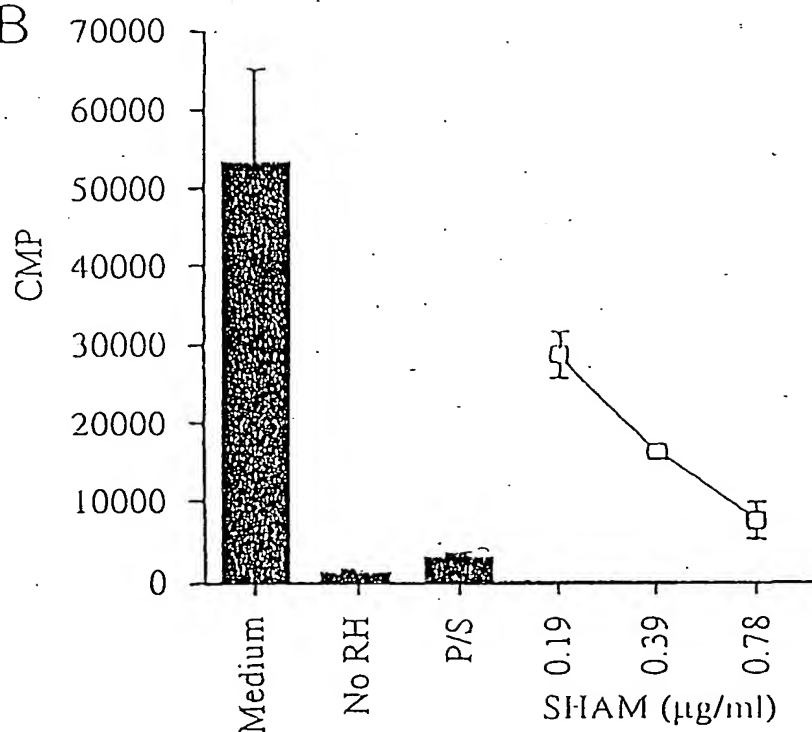


FIG. 4A

PHOSPHOENOLPYRUVATE + ERYTHROSE 4-PHOSPHATE

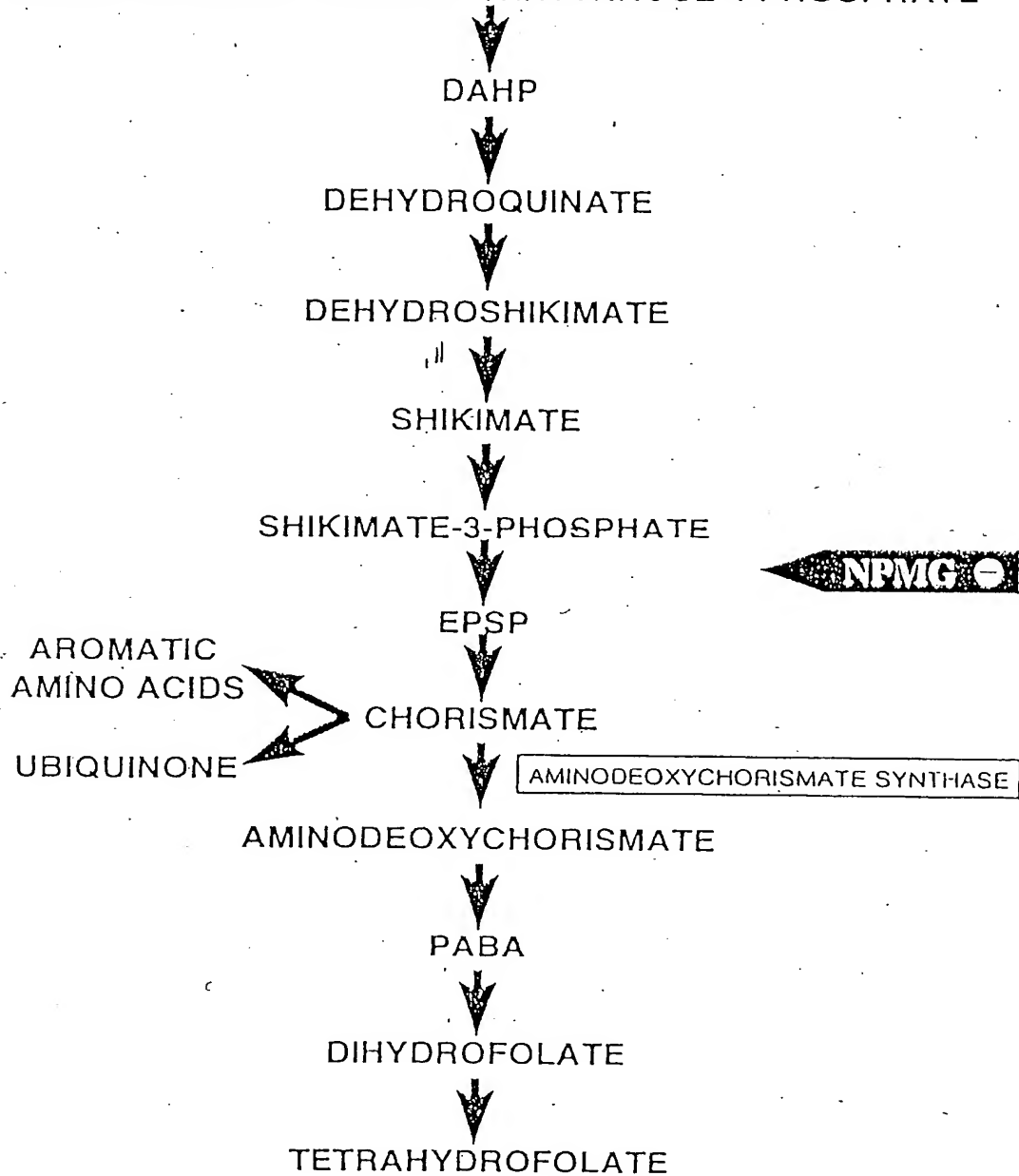


FIG. 4B

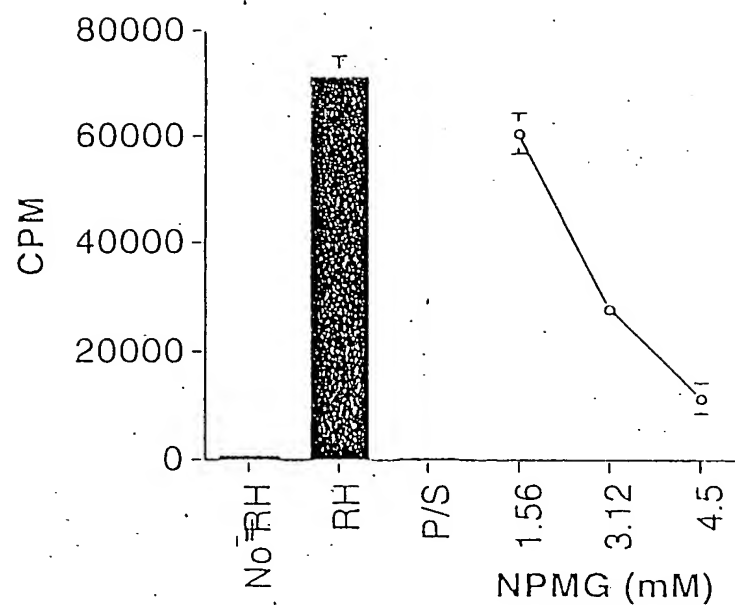


FIG. 4C

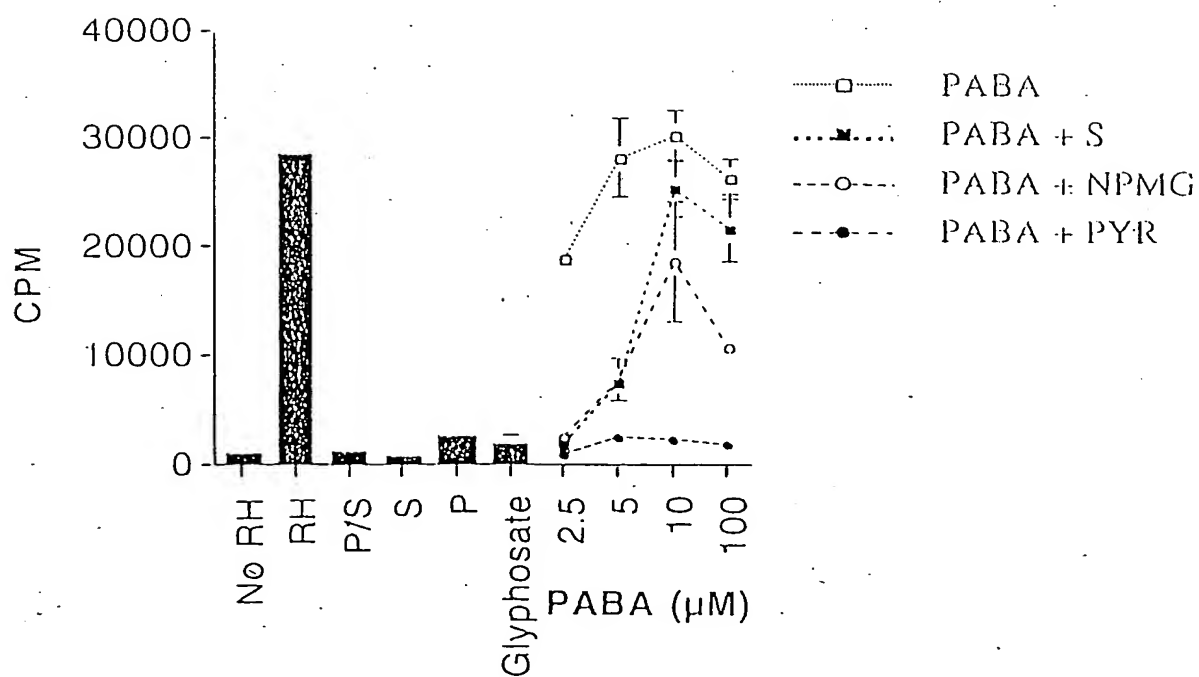


FIG. 4D

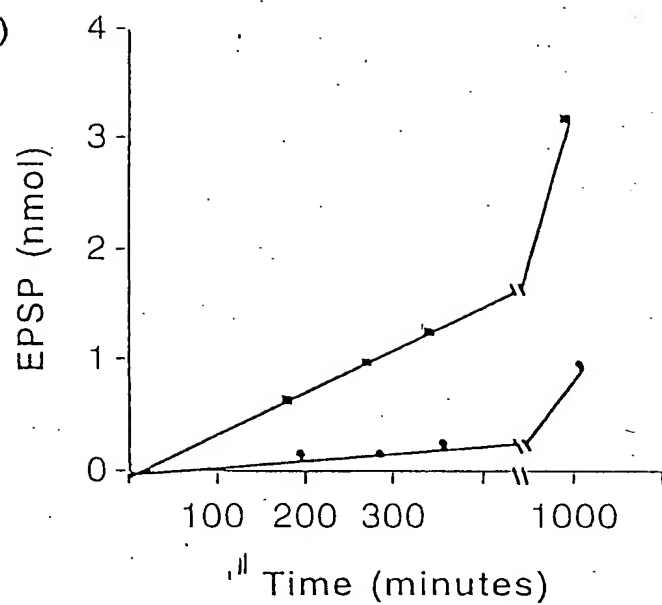


FIG. 4E

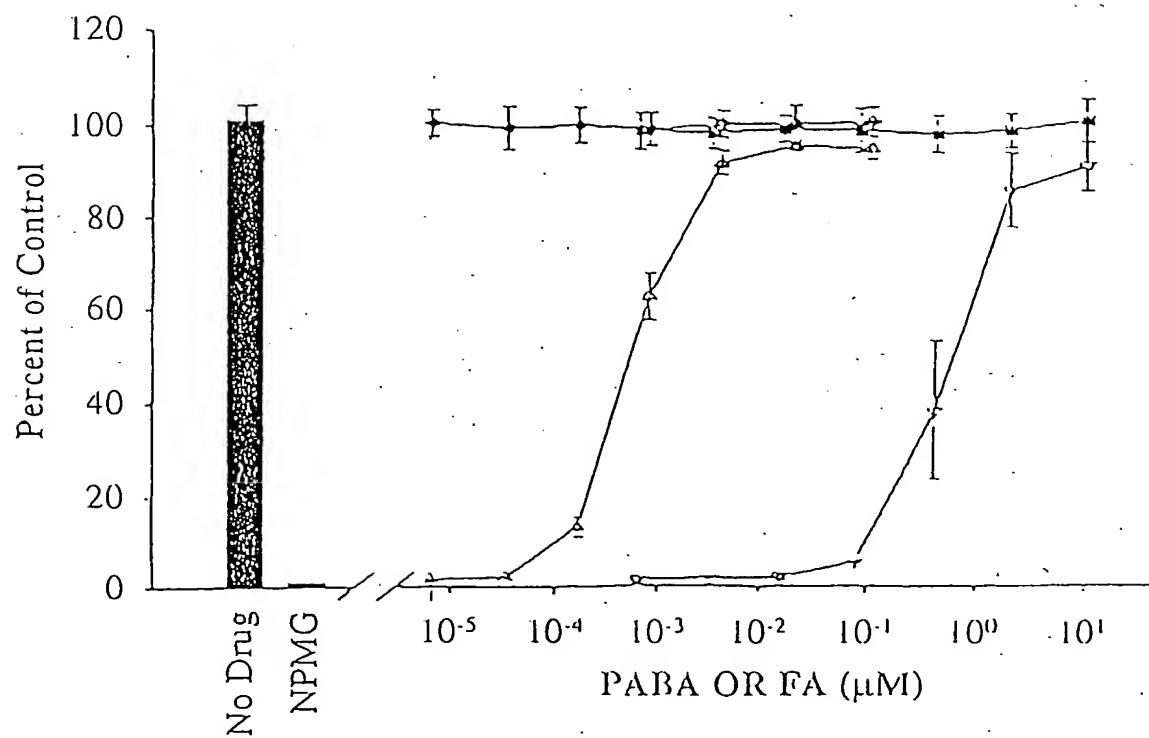


FIG. 5

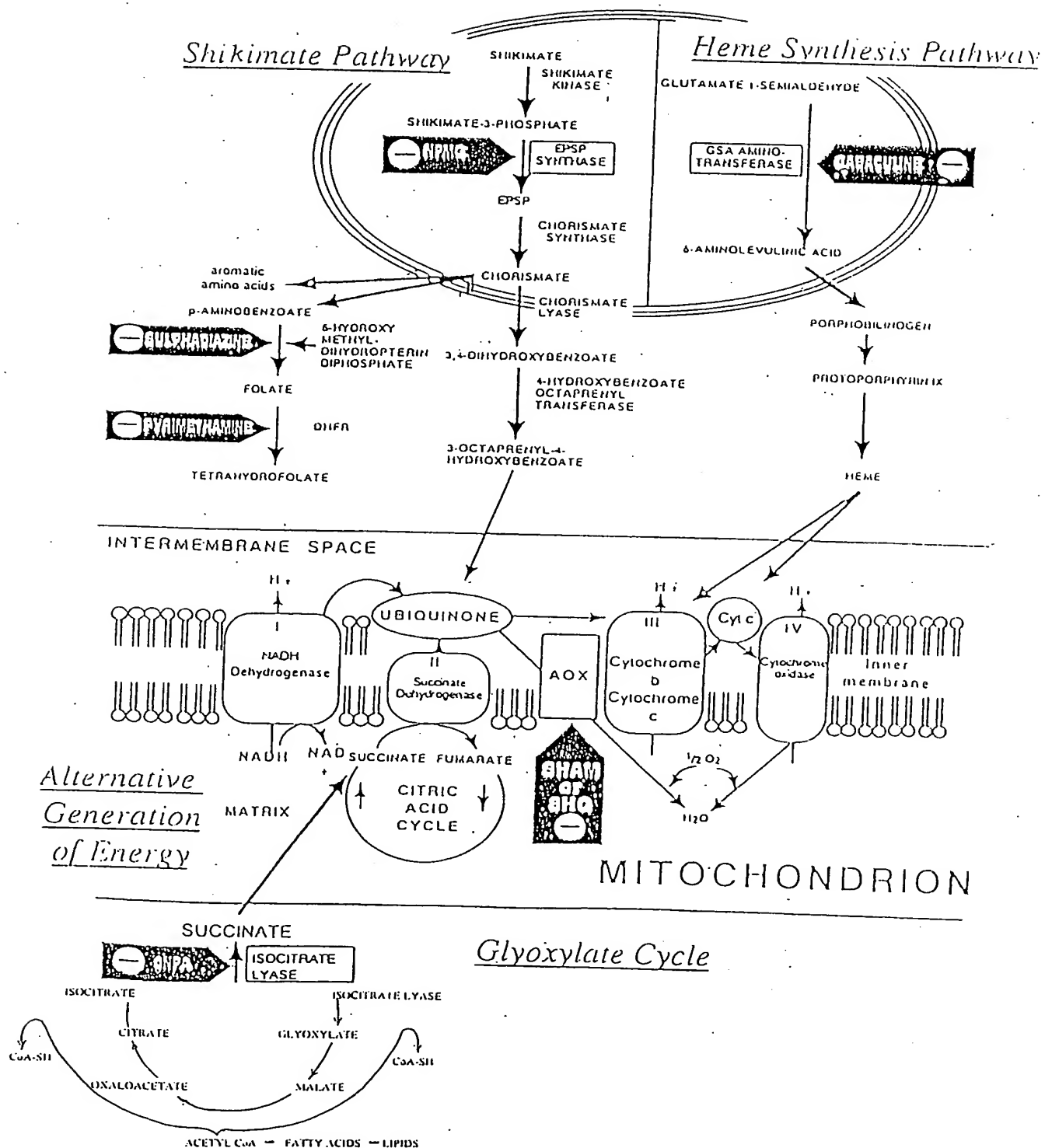


FIG. 6

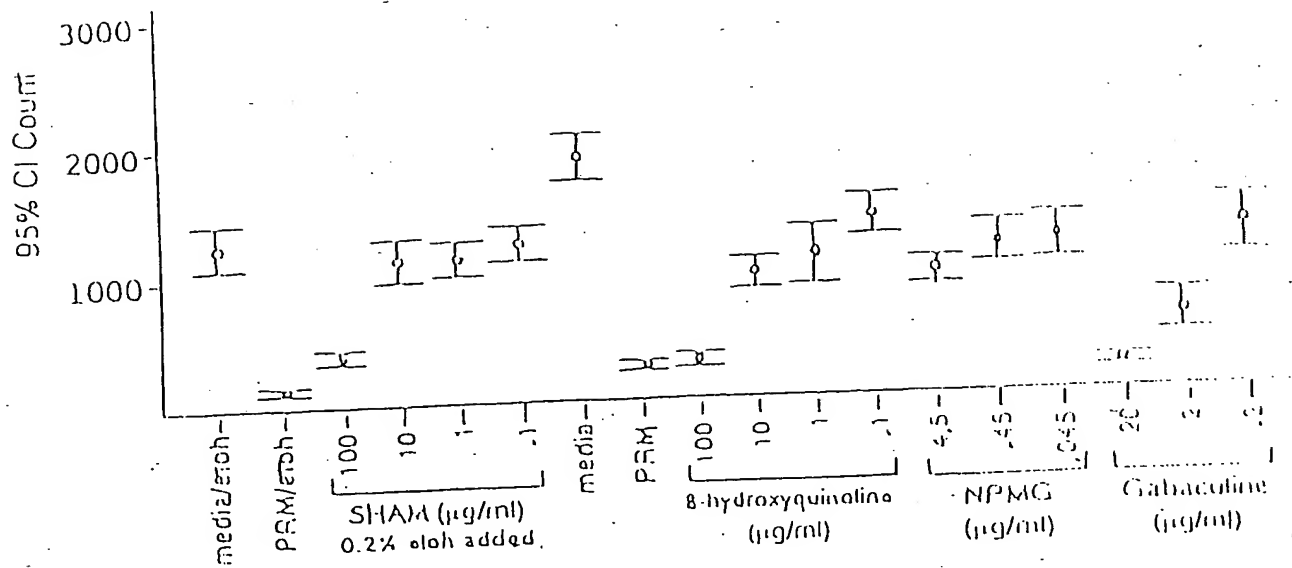


FIG. 7

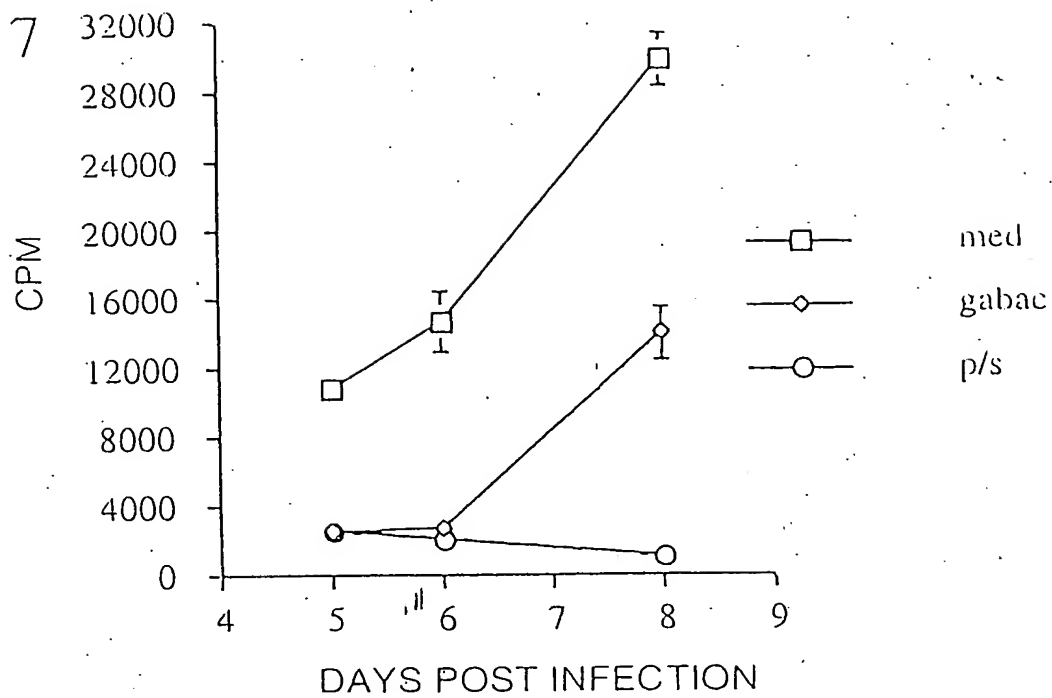


FIG. 8

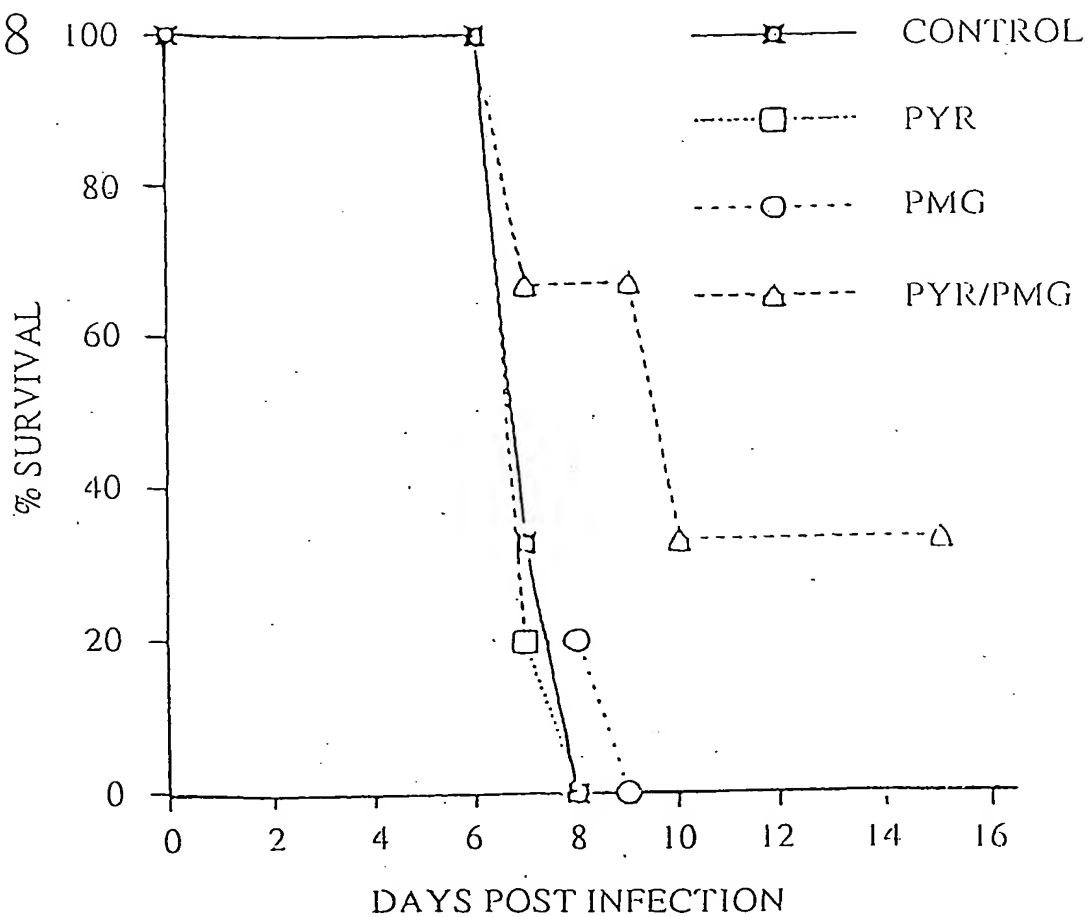


Fig. 9(1)

CT CAT CTT CTC GGT TTC	17
ACT TTT CTT TGA GTG CCT GTG TGA GAG ACG GTC GTC GCA ACA AGA ATC	65
TCC TCC GCT CAC GCC TTT CCT CAC AGT CCT GTT TTT CCT CCA GCT GTC	113
ACA CAT CCC GCT CGT TCC GCT GCA TCT CCT CAC ATT TCT TGC AGT CAG	161
ATG TCT TCC TAT GGA GCC GCT CTG CGC ATA CAC ACT TTC GGT GAA TCT	209
M S S Y G A A L R I H T F G E S	16
CAC GGC TCA GCC GTT GGG TGT ATA ATC GAC GGG CTG CCT CCT CGC CTC	257
H G S A V C C I I D G L P P R L	32
CCT CTT TCT GTC GAA GAT GTT CAG CCT CAA TTA AAT CGC AGA AGA CCC	305
P L S V E D V Q P Q L N R R R P	48
GGC CAA GGG CCT CTC TCG ACG CAG CGG AGA GAG AAA GAT CCA GTC AAC	353
G Q G P L S T Q R R E K D R V N	64
ATA CTC TCC GGT GTT GAA GAG GCA TAT ACA CTC GGT ACT CCC CTG GCG	401
I L S G V E D G Y T L G T P L A	80
ATG CTC GTC TGG AAT GAA GAC CGG CGG CCC CAG GAA TAC CAC GCC CTC	449
M L V W H E D R R P Q E Y H A L	96
GCG ACA GTC CCG CGT CCA GGT CAC GGG GAT TTC ACC TAC CAT GCA AAG	497
A T V P R P G H G D F T Y H A K	112
TAC CAC ATT CAC GCG AAA AGC GGG GCG GGT CGG AGC AGC GCG CGG GAG	545
Y H I H A K S G G G R S S A R E	128
ACT TTG GCG CGC GTC GCC GCT GGA GCA GTC GTT GAG AAG TGG CTA GGC	593
T L A R V A A G A V V E K W L G	144
ATG CAC TAC GGC ACC AGC TTC ACA GCT TGG GTC TGT CAG GTT GGT GAT	641
H H Y G T S F T A W V C Q V G D	160
GTC TCT GTG CCC CGA TCG CTC CGA AGA AAG TGG GAG CGG CAG CCG CCA	689
V S V P R S L R R K W E R Q P P	176
ACT CGC CAA GAC GTC GAT CGC CTT GCG GTC GTC CGC GTC AGC CCA GAT	737
T R Q D V D R L G V V R V S P D	192
GGA ACC ACA TTT CTC GAC GCG AAC AAC CGC CTT TAC GAC GAG CGA GGA	785
G T T F L D A N H R L Y D E R G	208
GAG GAA CTC GTC GAG GAG GAA GAC AAA GCC AGG CGT CGG CTT CTT TTC	833
E E L V E E E D K A R R R L L F	224
GGA GTC GAC AAC CCG ACG CCA GGA GAA ACA GTG ATT GAG ACC AGG TGC	881
G V D N P T P G E T V I E T R C	240
CCG TGC CCC TCC ACA GCT GTT CGC ATG GCT GTG AAA ATC AAC CAG ACC	929
P C P S T A V R H A V K I N Q T	256
CGA TCT CTG GGC GAT TCG ATT GGC GGA TGC ATC TCC GGT CCA ATC CTG	977
R S L G D S I G G C I S G A I V	272
CGG CCA CCG CTG GGC CTC GGC GAG CCG TGT TTC GAC AAA GTG GAG GCG	1025
R P P L G L G E P C F D K V E A	288
GAG CTG CCG AAG GCG ATG ATG TCG CTC CTT GCT ACG AAA GCG TTT GAG	1073
E L A K A M H S L P A T K G F E	304
ATT GGC CAG GGC TTT GCG AGT GTC ACG TTG CGA GGC AGC GAG CAC AAC	1121
I G Q G F A S V T L R G S E H H	320
GAC CGC TTC ATT CCC TTC GAG AGA CCG TCG TGT TCA TTC TCG GAA TCA	1169
D R F I P F E R A S C S F S E S	336
GCC GCG AGC ACG ATC AAG CAT GAA AGA GAT GGG TGT TCA GCT GCT ACA	1217

TO FIG. 9(2)

TO FIG. 9(1)

A	A	S	T	I	K	H	E	R	D	G	C	S	A	A	T	352
CTC	TCA	CGG	GAG	CGA	GCG	AGT	GAC	GGT	AGA	ACA	ACT	TCT	CGA	CAT	GAA	1265
L	S	R	E	R	A	S	D	G	R	T	T	S	R	H	E	368
GAG	GAG	GTG	GAA	AGG	GGG	CGG	GAG	CGC	ATA	CAG	CGC	GAT	ACC	CTC	CAT	1313
E	E	V	E	R	G	R	E	R	I	Q	R	D	T	L	H	384
GTT	ACT	GGT	GTA	GAT	CAG	CAA	AAC	GGC	AAC	TCC	GAA	GAT	TCA	GTT	CGA	1381
V	T	G	V	D	Q	Q	N	G	H	S	E	D	S	V	R	396
TAC	ACT	TCC	AAA	TCA	GAG	GCG	TCC	ATC	ACA	AGG	CTG	TCG	GGA	AAT	GCT	1409
Y	T	S	K	S	E	A	S	I	T	R	L	S	G	H	A	416
GCT	TCT	GGA	GGT	GCT	CCA	GTC	TGC	CGC	ATT	CCA	CTA	GGC	GAG	GGA	GTA	1457
A	S	G	G	A	P	V	C	R	I	P	L	G	E	G	V	432
CGG	ATC	AGG	TGT	GGA	AGC	AAC	AAC	GCT	GGT	GGA	ACG	CTC	GCA	GGC	ATT	1505
R	I	R	C	G	S	N	N	A	G	G	T	L	A	G	I	448
ACA	TCA	GGA	GAG	AAC	ATT	TTT	TTT	CGG	GTG	GCC	TTC	AAG	CCT	GTT	TCT	1553
T	S	G	E	N	I	F	F	R	V	A	F	K	P	V	S	464
TCC	ATC	GGC	TTG	GAA	CAA	GAA	ACT	GCA	GAC	TTT	GCT	GGT	GAA	ATG	AAC	1601
S	I	G	L	E	Q	E	T	A	D	F	A	G	E	H	H	480
CAG	CTA	GCT	GTG	AAA	GGC	CGC	CAC	GAT	CCC	TGC	GTC	CTT	CCG	CGA	GCC	1649
Q	L	A	V	K	G	R	H	D	P	C	V	L	P	R	A	496
CCT	CCT	CTG	GTT	GAG	AGC	ATG	GCT	GCC	CTT	GTG	ATT	GGC	GAT	CTG	TGC	1697
P	P	L	V	E	S	H	A	A	L	V	I	G	D	L	C	512
CTC	CGC	CAG	CGC	GCC	CGG	GAA	GGG	CCG	CAC	CCC	CTT	CTC	GTC	CTT	CCT	1745
L	R	Q	R	A	R	E	G	P	H	P	L	L	V	L	P	528
CAA	CAC	AGT	GGT	TGC	CCA	TCT	TGC	TGA	GCT	CTA	CCT	TGT	TCC	AAA	AAC	1793
Q	H	S	G	C	P	S	C									536
TTG	TGC	ATA	CGG	GGT	ACA	CCA	GGT	TCC	TCA	CAA	GGA	GAA	TCG	TGA	GGC	1841
GGT	GAC	TGG	CCA	GCG	CCA	CAG	ATT	GCT	GTT	CAT	GCA	CAA	GAA	AGA	AAA	1889
CAG	CGC	ATT	TCC	GCC	ACA	ACC	CAG	CTG	CAT	GAA	GTT	GCT	GGA	TAT	CGT	1937
TCC	GGC	GGT	GCT	CGG	CCT	TCT	TCT	CTA	CGC	TCG	CGA	TGA	TAC	GTC	GCG	1985
AGC	TTC	ATC	AAG	CTC	CTT	TTG	CAT	TGT	TAG	TGG	CTC	CCA	ACA	GAA	CCC	2033
TTT	GTG	GAA	GGG	AAT	CTG	GTC	TCA	CGC	TTG	CAG	GAG	AGA	GTT	CCC	CTT	2081
TGT	TCA	CGA	AAT	AAC	GAA	GCC	AAG	CAG	CTC	AGT	TGC	ATT	CAG	CCT	GCA	2129
CAC	AGT	TGC	ATT	CAG	CCT	GCA	CAC	TAA	ACA	CGG	GCG	AAA	TCG	TCG	CGT	2177
GAT	ATG	TAG	TTC	TTC	GGT	TGT	CAC	GGT	AAT	TGT	CGT	CGT	GTT	TGA	ACA	2225
ACT	AAA	CGT	TTC	TAA	TGC	TGG	ATC	TTA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	2273
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	2312

Fig. 9(2)

Fig. 10 (1)

T. gondii	-----MSSYGAALRIH	11
Synechocystis	-----HGNTFGSLFRIT	12
S. lycopersicum	MASSHLTKQFLGAPFSSFGSQQPSKLCSSHLRFPTHRSQPKRLEIQAGNTFGNYFRVT	60
N. crassa	-----MSTFGIYFRVT	11
H. influenza	-----MAGNTIGQLFRVT	13
S. cerevisiae	-----MSTFGKLFRT	11
T. gondii	TFGESHGSAVGGCIIDGLPPRLPLSVEDVQPQLNRRRPGQGPLSTQRREKDRVNIISGVED	71
Synechocystis	TFGESIHGGGVGVIIIDGCPRLLEISPEEIQVDLDRRRPGQSKITTPRKEADQCEILSGVFE	72
S. lycopersicum	TFGESIHGGGVGGCIIDGCPRLPLSESDMQVELDRRRPGQSRITTPRKETDTCKISSGTAD	120
N. crassa	TYGESHCCKSVGCIIDGVPPHCHMELTEDDIQPHTRRRPGQSAITTPRDEKDRVI IQSGTEF	71
H. influenza	TFGESHGIALGCIVDGVPPHLELSEKDIQPDORRKPGTSRYTTPRREDDEVQILSGVFE	73
S. cerevisiae	TYGESHCCKSVGCIIDGVPPHMSLLEADIQPOLTRRRPGQSKLSTPRDEKDRVE IQSGTEF	71
T. gondii	GYTLGTPLAMLVNEDRRPQEH--ALATVPRPGHGDFTYIAKYHIIAKSGGGRSSARET	129
Synechocystis	GKTLGTPIAILVRNKDARSQDYN--ENAVKYRPSHADATYEAKYGRIMQGGGRSSARET	130
S. lycopersicum	GLTTGSPIKVEVPNTDQRGNQYS--EMSLAYRPSHADATYDFKYGVRSVQGGGRSSARET	178
N. crassa	GVTLTGTPIGHLMVNEDQPPKDYCNKTMIDIYPRPSHADWTYLEKYGVKASSGGGRSSARET	131
H. influenza	GKTTGTSIGHIINQDQRSQDYG--DIKDRFRPGHADFTYQQKYGRDYRGCGGRSSARET	131
S. cerevisiae	GKTLGTPIANHIKNEQDRPHQYS--DMDKFRPSHADFTYSEKYGIKASSGGGRASARET	129
T. gondii	LARVAAGAVVEKHLGHYGTSTAWVCQVGDVSVPRSLRRKHERQPTRQDVDRLGVRV	189
Synechocystis	IGRVAAGATAKKILAQFNGVEIVAYVKS IQDIEA-----	164
S. lycopersicum	IGRVAAGAVAKKILKLYSGTEILAYVSQVIHVVLP-----	213
N. crassa	IGRVAAGATAEKYLKPRYCVIEIVAFVSSVSGSEHLFPPTAEHPSPST-----	177
H. influenza	AMRVAAGATAKKYLREHFGIEVRGFLSQIGNIKIAP-----	167
S. cerevisiae	IGRVASGATAEKFLAQNSHVEIVAFVTQIGFIKHIR-----	165
T. gondii	SPDGTTFLOANRLYDERGEELVEEEDKARRRLFGVDNPTPGETV IETRCPCPSTAVRH	249
Synechocystis	-----TVDSNTVTLEQVESN-----IVRCPDEECAEFH	192
S. lycopersicum	-----EDLVDMQIVTLEQIESN-----IVRCPHPEYAEKH	243
N. crassa	-----NPEFLKLVNSITRETVDNFL-----PVRCPDAAEANKRH	210
H. influenza	-----QKVGQIDWEKVNSN-----PFFCPDESAREKF	194
S. cerevisiae	DSFDPEFQIILLNTITREKVDSHG-----PIRCFDASVAGLM	201
T. gondii	AVKIHQTRSLGDSIGGCISGAIVRPPLGLGEPFDFVEAELAKAMHSLPATKGF EIGQGF	309
Synechocystis	IERIDQVLRQKDSIGGVVECAIRIAPKGLGEPVFOKLEADLAKAMHSLPATKGF EFGSGF	252
S. lycopersicum	IGADIVRVRGDSVGGVVTICIVRNVPRLGTPVFDKLEAELAKACHSLPATKGF EFGSGF	303
N. crassa	EDLITKFRDNHDSIGCTVTCVIRNVPSGLGEPAFDKLEAHIAHLSIPATKGF EFGSGF	270
H. influenza	DELIRELKKEGDSIGAKLTVIAENVPVGLGEPVFORLDADLAHALMGIAHVGVE ICDGF	254
S. cerevisiae	VKEIEKYRGKDSIGGVVTCVVRNLPTCLGEPFDFKLEAHIAHLSIPASEGF EIGSGF	261

TO FIG. 10 (2)

— TO FIG. 10(1) —

T.gondii	ASVTLRGSEIUNDRFIPFERASCSFSESAASTIKHERDGC SAATLSRERASDGRITTSRHEE	169
Synechocystis	AGTLLTGSQHND EYYIDEAGEWR-----	275
S.lycopersicum	AGTFMTGSEHNDEFFMDEHDQIR-----	326
N.crassa	GGCEVPGSIHNDPFVSAENTEIPPSVAASGAARNGI-----	306
H.influenza	AVVEQRGSEHRDEMTPNGFESNH-----	277
S.cerevisae	QGVSVPGSKINDPFYFEKETNR-----	283

T.gondii	EVERGRERIQRDTLIHVTGVDQONGNSED SVRYTSKSEASITRLSGNAASGGAPVCRIPLG	429
Synechocystis	-----	
S.lycopersicum	-----	
N.crassa	-----	
H.influenza	-----	
S.cerevisae	-----	

T.gondii	EGVRIRCGSHMAGGTLAGITSGENIFFRVAFKPVSSIGLEQETADFA-GENHQLAVKGRH	400
Synechocystis	-----TRTNRSGGVQGGISNGEPIIHRIAFKPTATIGQEOKTVSMI-GEETTLAAKGRH	328
S.lycopersicum	-----TKTNRSGGIQGGISNGEIIHNRVAFKPTSTIARKQHTVSRD-KHETELIARGRH	379
N.crassa	PRPKLTTKTNFSGGIQGGISNGAPIYFRVGFKPAATIGQEQTATYDGTSEGVLAAGRH	366
H.influenza	-----ACGILGGISSQPIIATIALKPTSSITIPGRSINLN-GEAVEVTKGRH	325
S.cerevisae	----LRTKTNNSGGVQGGISNGENIYFSVPFKSVATISQEOKTATYD-GEEGILAAGRH	330

T.gondii	DPCVLPRAPPLVESMAALVIGDLCLRQRAREGPHLLVLPQHSGCPSC-----	536
Synechocystis	DPCVLPRAVPHVEAMAAALVLCPIHLLRFQAQCKTL-----	362
S.lycopersicum	DPCVVPRAVPHVEAHVALVLVDQLMTQYAQCHLFPVHLLTQEPLQPSTTKSA-----	431
N.crassa	DPSVVPRAVPIVENMAALVIHDAVLAIHARVTAKSLLPLPKQTINSCKDTVCHGVSEHVG	426
H.influenza	DPCVGIRAVPIAEAHVAIVLLOHLLRFKAQCK-----	357
S.cerevisae	DPAVTPRAIPIVEAHVALVLADALLIQKARDFSRSVH-----	376

T.gondii	-----	
Synechocystis	-----	
S.lycopersicum	-----	
N.crassa	ESDLAQ	432
H.influenza	-----	
S.cerevisae	-----	

Fig. 10(2)

processing site

(SEQ ID NO: 55)

(SEQ ID NO: 13)

SCSFSESA5T1KHEDGCSA1TSLRPA5DRTISRHEEVEVG

11
Figs.

Fig. 12 (1)

McLeod *et al.*

CT CGA GTT															8	
TTT	TTT	TTT	TTT	TTT	TTT	TTG	ATA	CAT	AAT	AAT	CAA	GAG	TTC	TTT	ATA	56
CTA	ACA	GAC	TTA	TTT	AAT	GTA	TTA	TTT	TTG	GTA	AAC	AAA	AAA	AAC	ATT	164
ATG	AGC	ACA	TAT	GGG	ACT	TTA	TTA	AAA	GTA	ACA	TCC	TAC	GGA	GAA	AGT	152
M	S	T	Y	G	T	L	L	K	V	T	S	Y	G	E	S	16
CAT	GGG	AAA	GCT	ATT	GGG	TGT	GTG	ATC	GAT	GGG	TTT	TTA	TCC	AAT	ATA	200
H	G	K	A	I	G	C	V	I	D	G	F	L	S	N	I	32
GAA	ATA	AAT	TTT	GAT	TTA	ATA	CAA	AAA	CAA	TTA	GAT	AGA	CGA	AGA	CCA	248
E	I	N	F	D	L	I	Q	K	Q	L	D	R	R	R	P	48
AAT	CAA	TCA	AAA	CTA	ACT	AGT	AAT	AGA	AAC	GAA	AAA	GAT	AAA	CTT	GTT	296
N	Q	S	K	L	T	S	N	R	N	E	K	D	K	L	V	64
ATA	CTT	TCA	GGA	TTT	GAT	GAA	AAT	AAA	ACA	TTA	GGT	ACA	CCT	ATT	ACA	344
I	L	S	G	F	D	E	N	K	T	L	G	T	P	I	T	80
TTT	TTA	ATA	TAT	AAT	GAA	GAT	ATT	AAA	AAA	GAA	GAT	TAT	AAT	TCT	TTT	392
F	L	I	Y	N	E	D	I	K	K	E	D	Y	N	S	F	96
ATA	AAT	ATT	CCT	AGA	CCA	GGA	CAT	GGA	GAT	TAT	ACC	TAT	TTT	ATG	AAA	440
I	N	I	P	R	P	G	H	G	D	Y	T	Y	F	M	K	112
TAT	CAT	GTT	AAA	AAT	AAA	AGT	GGA	AGT	ACT	AGA	TTT	TCT	GGA	AGA	GAA	488
Y	H	V	K	N	K	S	G	S	S	R	F	S	G	R	E	128
ACA	GCC	ACA	AGA	GTT	GCT	GCT	GGG	GCG	TGC	ATT	GAA	CAA	TGG	CTT	TAT	536
T	A	T	R	V	A	A	G	A	C	I	E	Q	W	L	Y	144
AAA	TCT	TAT	AAT	TGT	TCT	ATT	GTT	AGT	TAT	GTA	CAT	TCA	GTT	CGG	AAT	584
K	S	Y	N	C	S	I	V	S	Y	V	H	S	V	G	N	160
ATA	AAG	ATA	CCT	GAA	CAA	GTC	AGC	AAA	GAA	TTG	GAA	AAT	AAA	AAT	CCA	632
I	K	I	P	E	Q	V	S	K	E	L	E	N	K	N	P	176
CCC	TCA	AGA	GAT	TTA	GTA	GAT	TCT	TAT	GGA	ACC	GTT	AGA	TAT	AAT	GAA	680
P	S	R	D	L	V	D	S	Y	G	T	V	R	Y	N	E	192
AAA	GAA	AAA	ATA	TTT	ATG	GAT	TGT	TTT	AAT	AGA	ATA	TAT	GAT	ATG	AAT	728
K	E	K	I	F	H	D	C	F	N	R	I	Y	D	M	N	208
GCT	TCT	ATG	TTA	AAA	ACT	GAT	GAA	TAT	AAT	AAA	AAC	ACA	TTG	ACT	ATT	776
A	S	M	L	K	T	D	E	Y	N	K	N	T	I	T	I	224
CCT	TCA	ATA	GAT	AAC	ACG	TAT	ATA	AAT	GTA	AAA	ACT	AAT	GAA	TGT	AAT	824
P	S	I	D	N	T	Y	I	N	V	K	T	N	E	C	N	240
ATA	AAT	CAG	GTT	GAT	AAT	AAT	CAT	AAC	AAT	TAT	ATT	AAT	GAT	AAG	GAT	872
I	N	Q	V	D	N	N	H	N	N	Y	I	N	D	K	D	256
AAC	ACT	TTT	AAT	AAT	TCT	GAA	AAA	TCG	GAT	GAA	TGG	ATT	TAT	TTA	CAA	920
H	T	F	N	N	S	E	K	S	D	E	W	I	Y	L	Q	272
ACA	AGA	TGT	CCA	CAT	CCA	TAT	ACT	GCT	GTA	CAA	ATT	TGT	TCT	TAT	ATT	968
T	R	C	P	H	P	Y	T	A	V	Q	I	C	S	Y	I	288
TTG	AAA	CTA	AAA	AAT	AAA	GGA	GAT	ACT	GTT	GGG	GGT	ATT	GCT	ACA	TGC	1016
L	K	L	K	N	K	G	D	S	V	G	G	I	A	T	C	394
ATT	ATA	CAA	AAT	CCT	CCT	ATA	GGT	ATT	GGA	GAA	CCT	ATT	TTT	GAC	AAA	1064
I	I	Q	H	P	P	I	G	I	G	E	P	I	F	D	K	320
TTG	GAA	GCT	GAG	CTA	GCC	AAA	ATG	ATT	TTA	TCT	ATT	CCA	CCC	GTG	AAA	1112
L	E	A	E	L	A	K	M	I	L	S	I	P	P	V	K	336

TO FIG. 12 (2)

TO FIG. 12 (1)

McLeod *et al.*

GGA	ATA	GAA	TTC	GGG	AGT	GGA	TTT	AAT	GGT	ACA	TAT	ATG	TTT	GGC	TCA	1160
G	I	E	F	G	S	G	F	N	G	T	Y	M	F	G	S	352
ATG	CAT	AAT	GAT	ATC	TTC	ATA	CCT	GTA	GAA	AAT	ATG	TCT	ACA	AAA	AAA	1200
M	H	N	D	I	F	I	P	V	E	N	M	S	T	K	K	360
GAA	AGT	GAT	TTA	TTA	TAT	GAT	GAT	AAA	GGT	GAA	TGT	AAA	AAT	ATG	TCT	1256
E	S	D	L	L	Y	D	D	K	G	E	C	K	N	M	S	384
TAT	CAT	TCA	ACG	ATT	CAA	AAT	AAT	GAG	GAT	CAA	ATA	TTA	AAT	TCA	ACT	1304
Y	H	S	T	I	Q	N	N	E	D	Q	I	L	N	S	T	400
AAA	GGA	TTT	ATG	CCT	CCT	AAA	AAT	GAC	AAG	AAT	TTT	AAT	AAT	ATT	GAT	1352
K	G	F	H	P	P	K	N	D	K	N	F	N	N	I	D	416
GAT	TAC	AAT	GTT	ACG	TTT	AAT	AAT	AAT	GAA	GAA	AAA	TTA	TTA	ATT	ACA	1400
D	Y	N	V	T	F	N	N	N	E	E	K	L	L	I	T	432
AAA	ACA	AAT	AAT	TGT	GGT	GGG	ATT	TTA	GCT	GGC	ATT	TCA	ACA	GGA	AAC	1448
K	T	N	N	C	G	G	I	L	A	G	I	S	T	G	N	448
AAT	ATT	GTT	TTT	AGA	TCA	GCA	ATC	AAA	CCT	GTA	TCA	TCA	ATA	CAA	ATA	1496
N	I	V	F	R	S	A	I	K	P	V	S	S	I	Q	I	464
GAA	AAA	GAA	ACA	AGT	GAT	TTT	TAT	GGA	AAT	ATG	TGT	AAC	TTG	AAA	GTT	1544
E	K	E	T	S	D	F	Y	G	N	M	C	N	L	K	V	480
CAA	GGG	AGA	CAT	GAT	AGC	TGT	ATT	TTA	CCA	AGA	TTA	CCA	CCC	ATT	ATT	1592
Q	G	R	H	D	S	C	I	L	P	R	L	P	P	I	I	496
GAA	GCA	TCT	TCT	TCA	ATG	GTT	ATA	GGA	GAT	TTA	ATA	TTA	CGA	CAA	ATA	1640
E	A	S	S	S	M	V	I	G	D	L	I	L	R	Q	I	512
TCA	AAG	TAT	GGA	GAT	AAA	AAG	TTG	CCA	ACA	TTG	TTT	AGG	AAT	ATG	TAA	1608
S	K	Y	G	D	K	K	L	P	T	L	F	R	N	M		527
CAT	AAT	GAT	TTT	GTA	ATC	CTC	AAT	TAA	AAT	GAA	AAA	TTA	TAA	AAT	ATA	1726
TAT	TTT	ATA	TAT	ATA	TAT	AAA	ATA	TAT	ATA	TAT	ATA	TAT	AAA	ATA	TAA	1784
ATA	TAT	GTA	TAA	TAA	TTC	AAT	TTG	CGC	AAT	CGA	TCA	AAA	TAC	ATT	TGC	1832
TCT	AC															1837

Fig. 12 (2)

FIG. 13 (1)

GAATTCTGCAGTTCTCTCGAATATATGGCTGCCCACTACCCGTAGGTATT 50
TGCACGACGACGCTTGCGTCACTCGGCGGCGTGACACACAACCTGCACTG 100
GCCGCCACTCGCGCGCATCCACGGTAGAGCTAACGAGTCTGCGATGGGGT 150
TAGAGACGCACACCTTTGACTCCCCGGGGCCTACGGAGACGACGCGGACGC 200
GTGTCTCCCCCTTTTCGCTCTTTTACTGTACGCTGGTAAAACGACTTTTC 250
GACGCAGCATGGTTCTCATCTTCTCGGTTTCACTTTTCTTTGAGTGCCTG 300
TGTGAGAGACGGTCGTGCGAACAAGAATCTCCTCCGCTCACGCCTTTTCCT 350
CACAGTCCTGTTTTTTCCTCCAGCTGTACACATCCCGCTCGTTCCGCTGC 400
ATCTCCTCACATTTCTTGCAGTCAGATGTCTTCCTATGGAGCCGCTCTGC 450
GCATACACACTTTCGGTGAATCTCACGGCTCAGCCGTTGGGTGTATAATC 500
GACGGGCTGCCTCCTCGCTCCCTCTTTCTGTGCGAAGATGTTACGCCTCA 550
ATTAAATCGCAGAAGACCCGGCCAAAGGGCCTCTCTCGACGCAGCGGAGAG 600
AGAAAGATCGAGTCAACATACTCTCCGGTGTGGAAGACGGATATACACTC 650
GGTGAGGGAAGAACTACAGACGTCACGTGCCTGTGCCAGCACATAACTG 700
CAGATTCATATATATATATACATATACAGATGTGTATTTTGTGTGTATAG 750
TTAAGCAGAGGATGGTATTGAAAATGGCTGTGCGGTGTATTCTTATTCGCC 800
CTGTGGCGCTTTTGGAGAAGGCCCTGGGGAAACGGAAGCCCTGGCACAAG 850
GGCTGCCGGCTAAGCTTCAGAAACCGCAGTTAATAGCTCGAAAGTACCGT 900
ATCCAAACGTTCTCTTTTATCCACACAGTGTGTTGGACACAAGCGAAGCC 950
GAAAAGTGTCTTGCACGTGGCGAGTTTTTCGGTGACAAAACACACGCGCCA 1000
CTCCGTAGAAATACCGGATCCGAGTTTACCTGCTGCAGGCTTCGGAACGC 1050
TGCTTTGTTCCGAAGATGGCCTCGTGGTTTCGATGGGAAATTGGAGGGTG 1100
CAAAAGTGCCCGGCGCTCGTGGCCTGCGCCATCTGGCATCGTGGACTGGC 1150
CGTCTACCGTGATCCTCGCGTCCCTTCCAAAAAATCATTTTTTCTCTGCTT 1200
CGCCTTCTCGTTTCGTGTCACCGGGATCCGTCTGCAGGTACTCCCCTGGCG 1250
ATGCTCGTCTGGAATGAAGACCGGCGGGCCCCAGGACTACCACGCCCTCGC 1300
GACAGTCCCGCGTCCAGGTCACGGGGATTTACCTACCATGCAAAGTACC 1350
ACATTCACGCGAAAAGCGGGGGCGGTCTGGAGCAGCGCGCGGGAGACTTTG 1400
GCGCGCGTCCCGCTGGAGCAGTCTGTTGAGAAGTGGCTAGGCATGCACTA 1450
CGGCACCAGCTTCACAGCTTGGGTCTGTGAGGTGAGACGAAGCCCAGAAG 1500
GTTCACAGCAGAGTGGATGAAAGACAGAGATAGACAGGTCTTCCCTGGAG 1550
GCAGTACGCGGATGGAAGACAACGTTACGGCGCTTTCCGATTCATGGGGC 1600
AAGCGTGGCTAAATTTTCCATGACTCGACAGCGGTGACCCTAGGATCGCGT 1650
CGGTTTTTGATGCCTGGTTCCTCTCACGCCCTTAGGTTGGTGATGTCCTCTG 1700
GCCCCGATCGCTCCGAAGAAAGTGGGAGCGGCAGCCGCCAACTCGCCAAG 1750
ACGTCGATCGCCTTGGCGTGGTCCGCGTGAGCCCAGATGGAACCACATTT 1800
CTCGACGCGAACAACCGCCTTTACGACGAGCGAGGAGAGGAACTCGTCCA 1850
GGAGGAAGACAAAGCCAGGCGTCGGCTTCTTTTCGGAGTCGACAACCCGA 1900
CGCCAGGAGAAACAGTGATTGAGACCAGGTGCCCGTGCCCCCTCCACAGCT 1950

FROM FIG. 13 (1)

FIG. 13 (2)

GTTTCGCATGGCTGTGAAAATCAACCAGGTGAGGTGGAGCAGTGCGATGAG 2000
CCATCTGTTCACTGGATCCGTAAACGCGAAGGTCATCCGTGGGGGAAAAA 2050
AGTGAATCTACGGAAGGTGAGCTGGCTTTGGCCGTGACACGTCTAGTCTA 2100
CCCTGCAGACCTACCATTGCGGAATAGCAAAGCAGCGGGGAAGGCGTC 2150
ACCCGGAGAAGGGTGTGAGCAGTGCGCCACCCAGAGGCTCGGAAGACC 2200
TCCGCGAACGTTGATGGTGTGCACGGTGCGGTACCTTTCAGCGGCGAAAC 2250
CCTCCATCCGAGTGTGCAGACAAGTCATCACCCAGTTGTATGAAGCACC 2300
CTGCCTTCGATGGTGTCCCTACTTTATCCTCTCAGACCCGATCTCTGGGC 2350
GATTCGATTGGCGGATGCATCTCCGGTGCAATCGTGCGGCCACCGCTGGG 2400
CCTCGGTAAAGCAGTCTCGTTTTCTGTGTTCCTCGGCTCCTATACAGCAC 2450
CTGACCACGTTTCTAGGTGGTGTGGCGACAGGTCGGACCTATATTCGAGA 2500
CGTGACAGTTCGTCCAAATTGCTCGTTCATGCACCAGCATCTCCTTGC 2550
CAGACACCCACACACCGCATAGGTTTGCTTGACAAATGAAACTGACAAA 2600
TACGACCTGCGGGGACTTGTGACAACGTTGCCCTTTTGCCGTTTTCTCTGC 2650
GAGGTCGTGACTGAGGCGCTGGTGAAGAGCGAGACTGGGCCGAGGCGTGT 2700
GTTTCCATGCAAACAGAAAGCAGGCTGATAGAGACAATGCAAACGAGCGGA 2750
CGTGGAAGCGCAGTGTGTAATGCATGAACTAAAGGTGCACACACCT 2800
GCGCACCAACCCGAGATGCAGCGACCGACGGCACACCTCTGTGAGGTGCAG 2850
ATGACTCTGCATCAAGAATCAGTGCCTCAGAGACCCTTTTCCCCGTGTAG 2900
TTTCTCAGTGCGGCAGAAAGAGTTTTTCGTTGCTCTGTTTCAGTCCATCCAC 2950
CACCAGCAGTTGGCGCCAACCTGCGAGACCGAGAAGGCAGCATGCGAGAAT 3000
TCAGAGAGTGCAAGGGAGAGTTTTTTGAATCATGTTTTCTCTGATTTCTT 3050
GCTGGAGGTCTGTGCATGTAGGCGAGCCGTGTTTCGACAAAGTGGAGGCG 3100
GAGCTGGCGAAGGCGATGATGTCGCTCCCTGCTACGAAAGGGTTTGAGGT 3150
ATGTGTGCAACTTTCTCCAGAGAGGTGATAATTGAGCACGACGCATGCAA 3200
TTTGTGGTCAGGCCCAATATGTACAGCTCAGTTTCCACCGAAGAAATCAA 3250
CACTGGTCGGGTCTTTTTCAGCCACCTGTGGCCGTGTCGCTTTCACCTCTT 3300
GCCTGGGATAGATGTGAGGCACACTTCGTCAACACCTTGCCGCTGGCTCT 3350
ATATCGGACGCCACCCTGAAATCGCGTTGCGAATGTTTTCTTTTGCATTTCC 3400
TGATGCATCCGTCTGTGTGTGACAGATTGGCCAGGGCTTTGCGAGTGTTCAC 3450
GTTGCGAGGCAGCGAGCACAAACGACCGCTTCATTCCCTTCGAGAGAGCGT 3500
CGTGTTTCACTCTCGGAATCAGCCGCGAGCACGATCAAGCATGAAAGAGAT 3550
GGGTGTTACGCTGCTACACTCTCACGGGAGCGAGCGAGTGACGGTAGAAC 3600
AACTTCTCGACATGAAGAGGAGGTGGAAGGGGGCGGGAGCGCATACAGC 3650
CGGATACCCTCCATGTTACTGGTGTAGATCAGCAAAACGGCAACTCCGAA 3700
GATTCAGTTCGATACACTTCCAAATCAGAGGCGTCCATCACAAGGCTGTCT 3750
GGGAAATGCTGCCTCTGGAGGTGCTCCAGTCTGCCGCATTCACCTAGGCG 3800
AGGGAGTACGGAATCAGGTGTGGAAGCAACAACGCTGGTGGAACGCTCCGA 3850
GGCATTACATCAGGTGGGTCCCGACCCGTTACTCGCGCTCCGCTTCTCTCT 3900

FIG. 13(3)

CCAGTTCGGCGTTTCGACAGCACTCGTTCAAAGTG GTTGGT TTTCTGGCC 3950
 AGTGGCAGCATTGGCTGTAAAGAACACACTGTTGCTGGCTGCTTTCAATA 4000
 GGTGTAAAAAACTGGTGTCTTTTCATTCAGTCTACAGCTCTGATGCAC 4050
 CTTTCTGGTGCCACGTGAGTCCTTGCTGCGGCCATCGACTCAGATAGAA 4100
 CAAGATCCCCCAGATACAAGAGAAATGTCTTGAGCCAAGAAGACGGCTGT 4150
 CTAATTACACGATACGGACATCAGTAATGAGATTTTAACAGAGGGGCTTC 4200
 CAGCATCGCTGCAGGATGTCGCGTCGCGACCTCAGGTTGTGTGATTCTGTG 4250
 CTGAGAGACACACATTGTGCAACTGCTGCCTGCCCTGTCTTGTTCGTGCG 4300
 TCCGTGGTGAAGTACCATCGACGTGATGAACAGCCTGAATGCAGACGTGC 4350
 TCTAACGGGGTGCGCACCAACCCCAAGAGGACGGTGTGACTACGTCCGTGG 4400
 CGTGGAATTGATGTGTGTTCATCAGGAGAGAACATTTTTTTTCGGGTGGCC 4450
 TTCAAGCCTGTTTCTTCCATCGGCTTGGAACAAGAACTGCAGACTTTGC 4500
 TGGTGAAATGAACCAGCTAGCTGTGAAAGGTAAGAGGCATTTGCTTATTT 4550
 GGGTCTCGACTTAGGCGGTACATTTCCATTCACTCTTATCAACATTTGC 4600
 AAGGTCGAAATCTGTGGTGCACATGGATGCAGTCGAGGGCGGGTCACTCA 4650
 CATTCGATTTTCTCCACACGCTCGCCCAACAAGAACTGGTTTGGTGTTC 4700
 TCGTGAATTCTGTGACAGGCCGCCACGATCCCTGCGTCCCTCCGCGAGCC 4750
 CCTCCTCTGGTTGAGAGCATGGCTGCCCTTGTAAGCCGGCAACATAATCT 4800
 GGGAAAACGAAAACGATTGCCAGAGCGGGGATGGGCACAACACGGATCCG 4850
 TGATGTTCCGTAGTACCTCGAGTCTCTCTGAGTCTTGTGCGGGATTGGTG 4900
 ACTGCACCCAAAATGTGTTGGAATCGAACGCTGGATCAGTGAACCTCCTTG 4950
 GCTGATGTCTCTCAACCGTATGACTGCTTCTCAAACAGCTCATATAACAC 5000
 CCGTGCGGAAGTGTAGCAACAATTTTCCTTCACAATTTGGCCCCGGGTCCGT 5050
 GCAAAGACATTATGCAAAGCAGCCCTCAGTCGTGTGCCTCGCTTGCGTGC 5100
 AGTTTCACGTAAGACTGGCATGAGGACCGAACTACCGTGCAGGGAAACAT 5150
 GCTGACGTCCCCCGTAGAATGTTCTTGAGGGAACTGCGGGTGTGGCCCTCC 5200
 TTTCCTCGAACAGTAGGACAATCCTGTCTTCTTGTGCGCTTGTAGATCCTTG 5250
 CCGTTTCATTAAACCCCTCTTTGAATTTCGTCACTTGCCTCGATGACATGTC 5300
 CCTTAGGTGATTGGCGATCTGTGCCTCCGCCAGCGCGCCCGGGAAGGGCC 5350
 GCACCCCCCTTCCTCGTCCCTTCCTCAACACAGTGGTTGCCCCATCTTGCCTGAC 5400
 CTCTACCTTGTTCCAAAAACCTTGTGCATACGGGGTACACCAGGTTCCTCA 5450
 CAAGGAGAATCGTGAGGCGGTGACTGGCCAGCGCCACAGATTGCTGTTCA 5500
 TGCACAAGAAAGAAAACAGCGCATTTCCGCCACAACCCAGCTGCATGAAG 5550
 TTGCTGGATATCGTTCCGGCGGTGCTCGGCCTTCTTCTCTACGCTCGCGA 5600
 TGATACGTGCGGAGCTTCATCAAGCTCCTTTTGCAATTGTTAGTGGCTCCC 5650
 AACAGAACCCTTTGTGGAAGGGAATCTGGTCTCACGCTTGCAGGAGAGAG 5700
 TTCGCCTTTGTTACGAAATAACGAAGCCAAGCAGCTCAGTTGCATTCAG 5750
 CCTGCACACAGTTGCATTCAGCCTGCACACTAAACACGGGCGAAATCGTTC 5800
 GCGTGATATGTAGTTCTTCGGTTGTACGGTGATTGTGCTCGTGTTCGAA 5850

FROM FIG. 13 (3)

FIG. 13 (4)

CAACTAAACGTTTCTAATGCTGGATCCGAATTC

5883

FIG. 14A

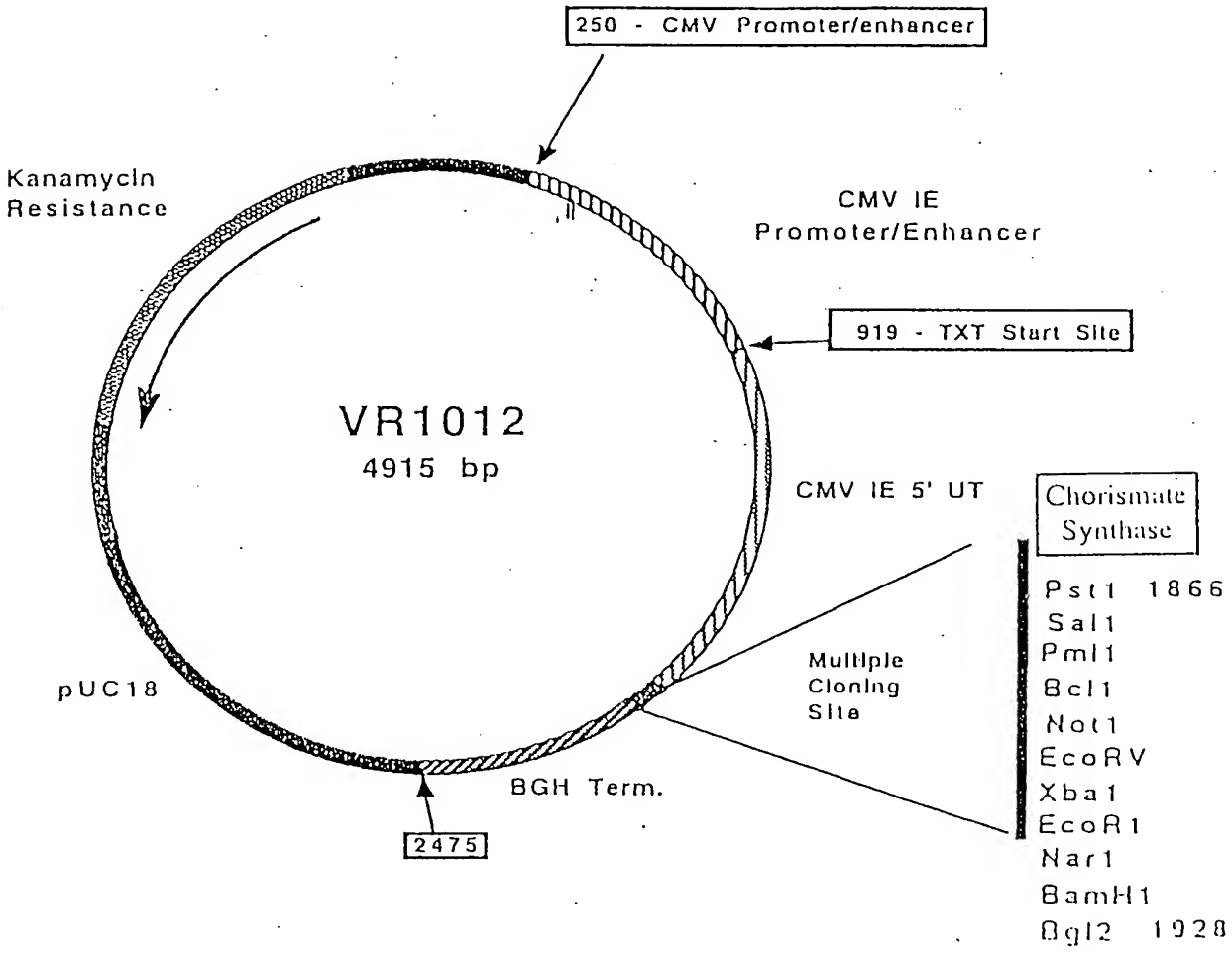
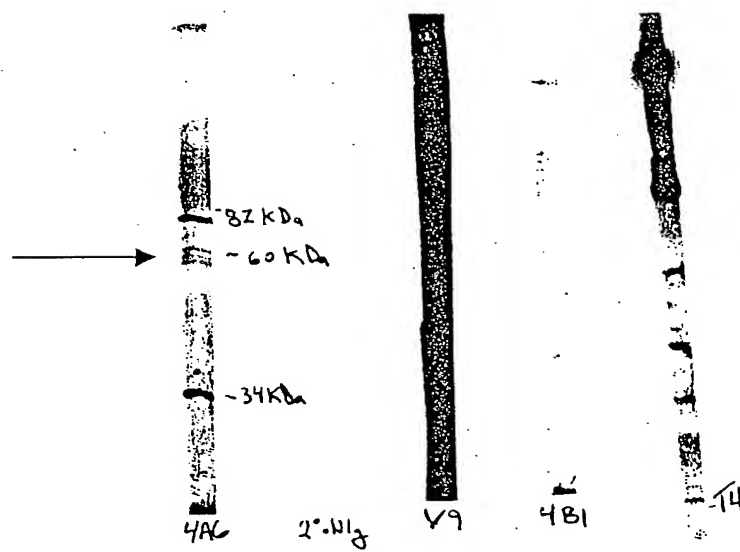


FIG. 14B



Key: —————> Indicates Chorismate Synthase

FIG 15

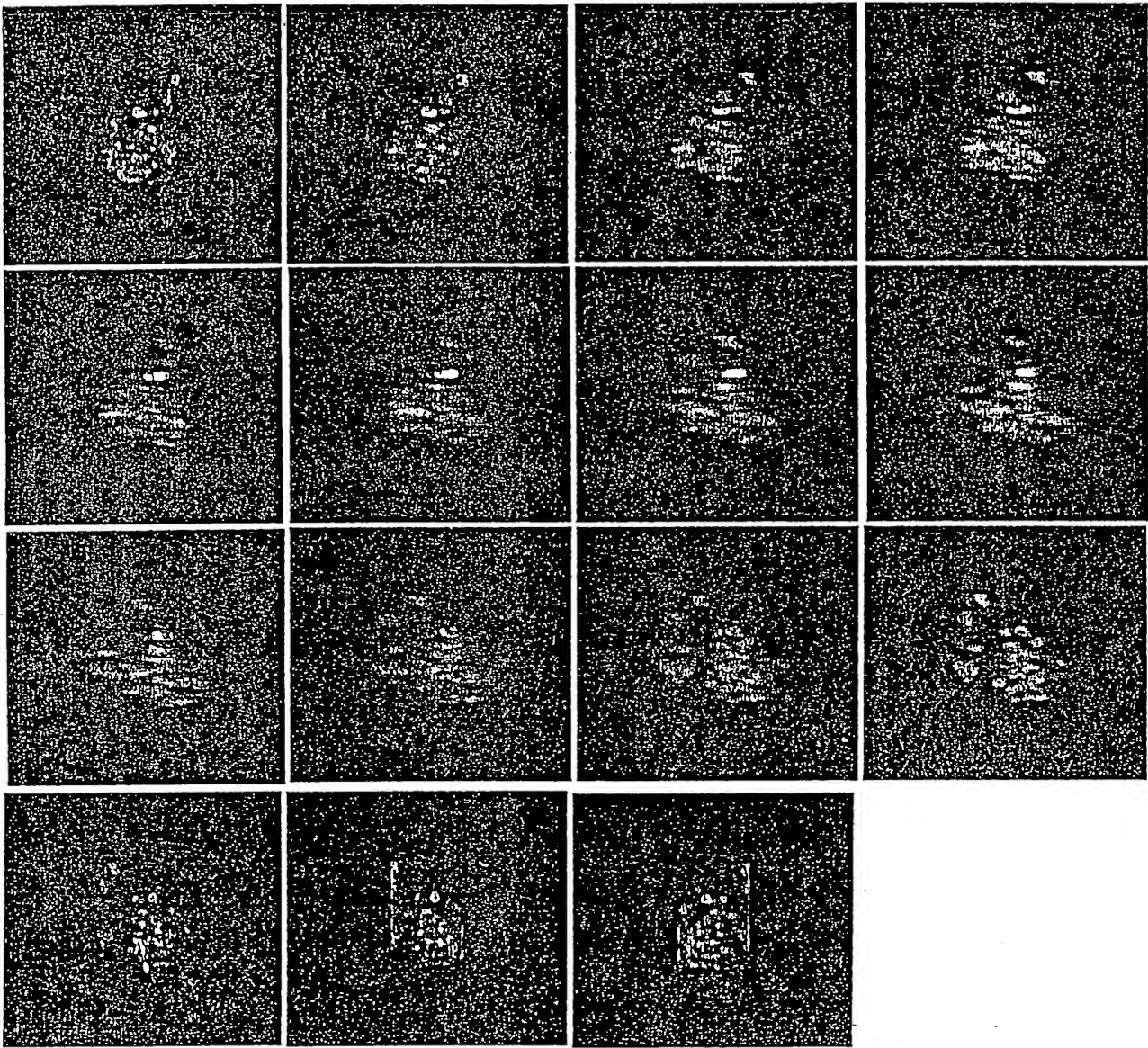


FIG 16A1

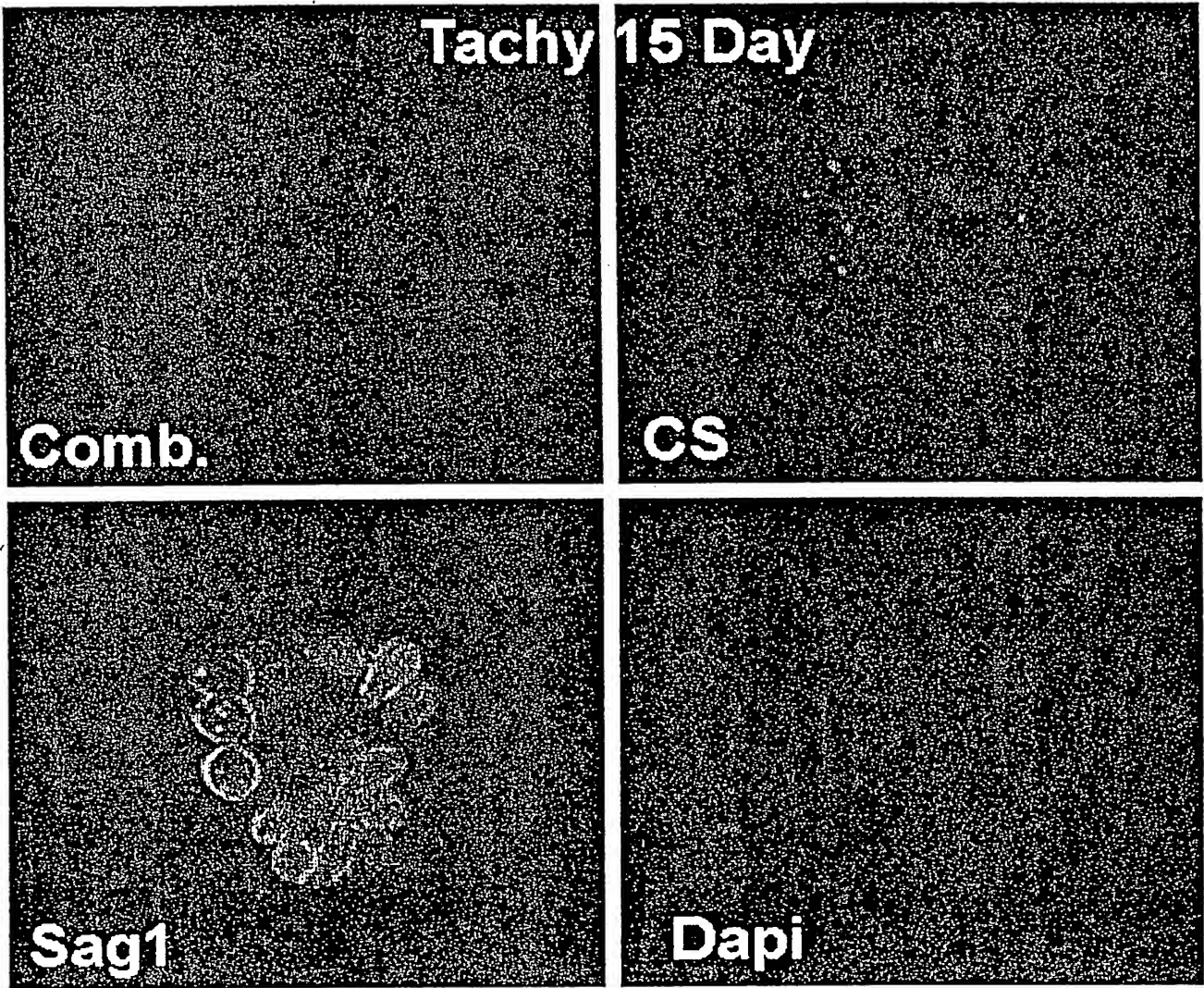


FIG 16A2

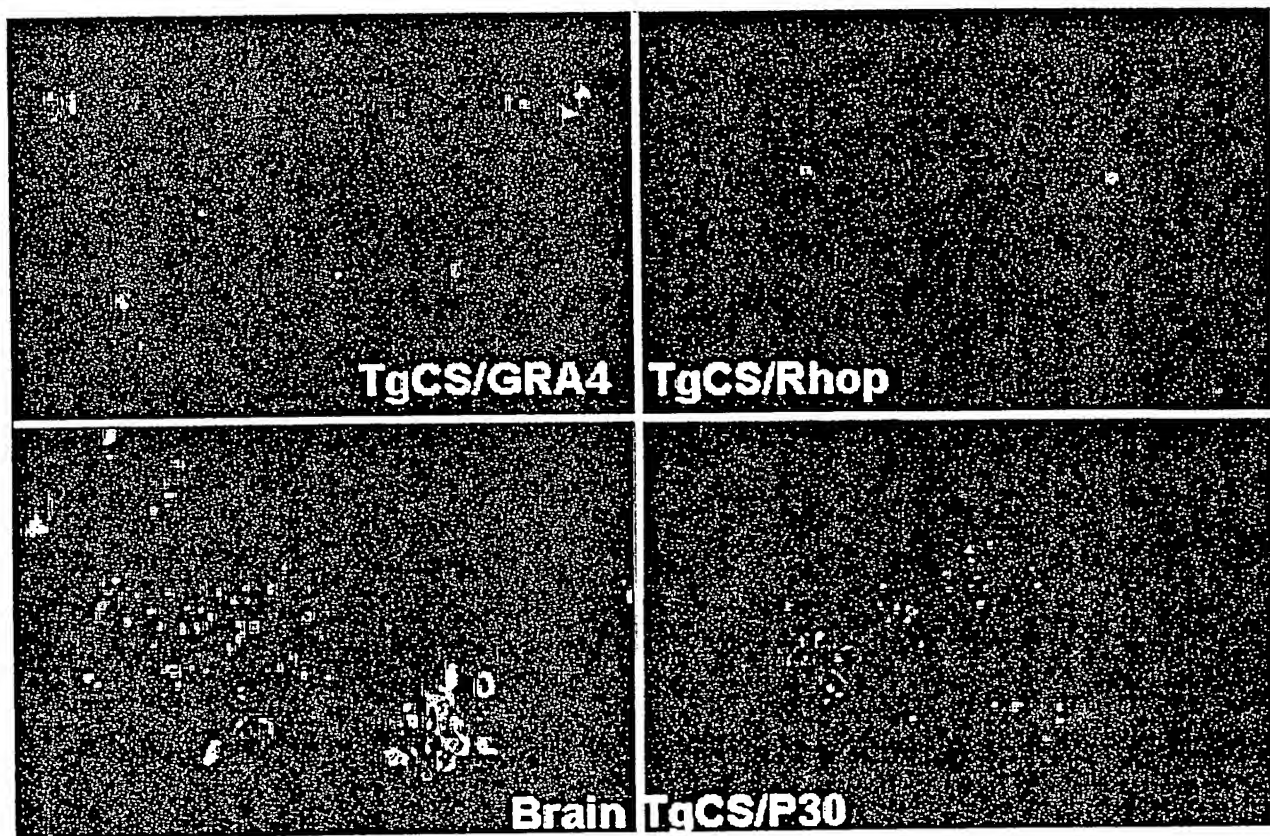


FIG 16A3

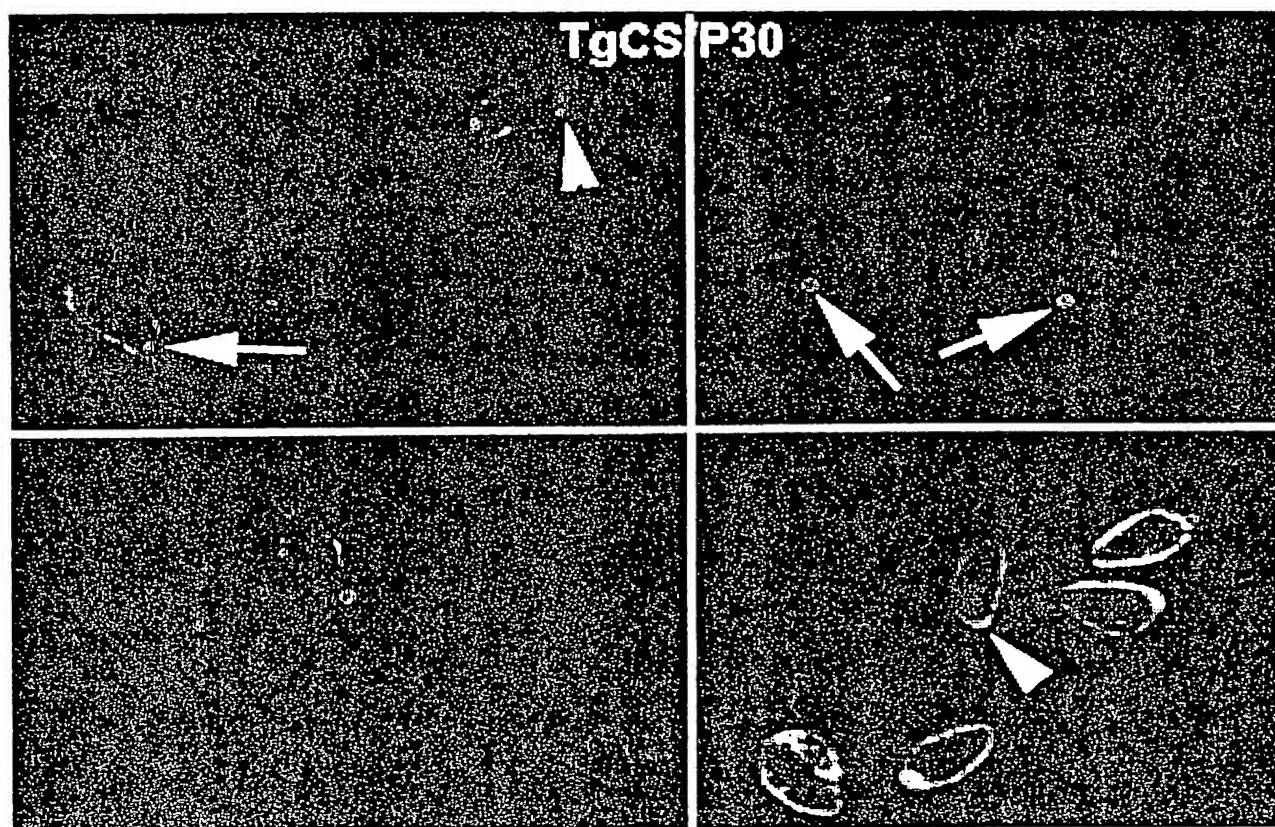


FIG 16B1

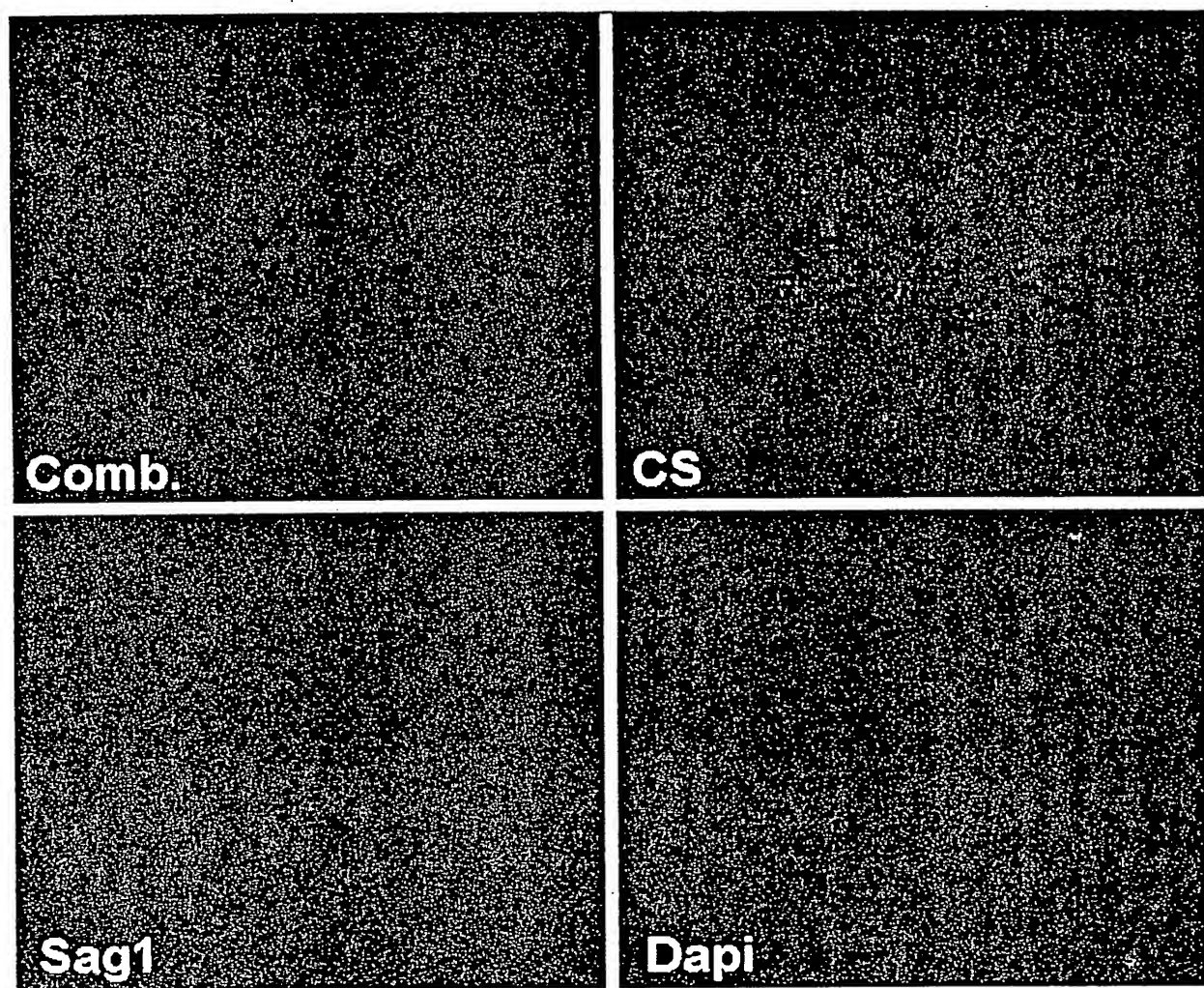


FIG 16B2

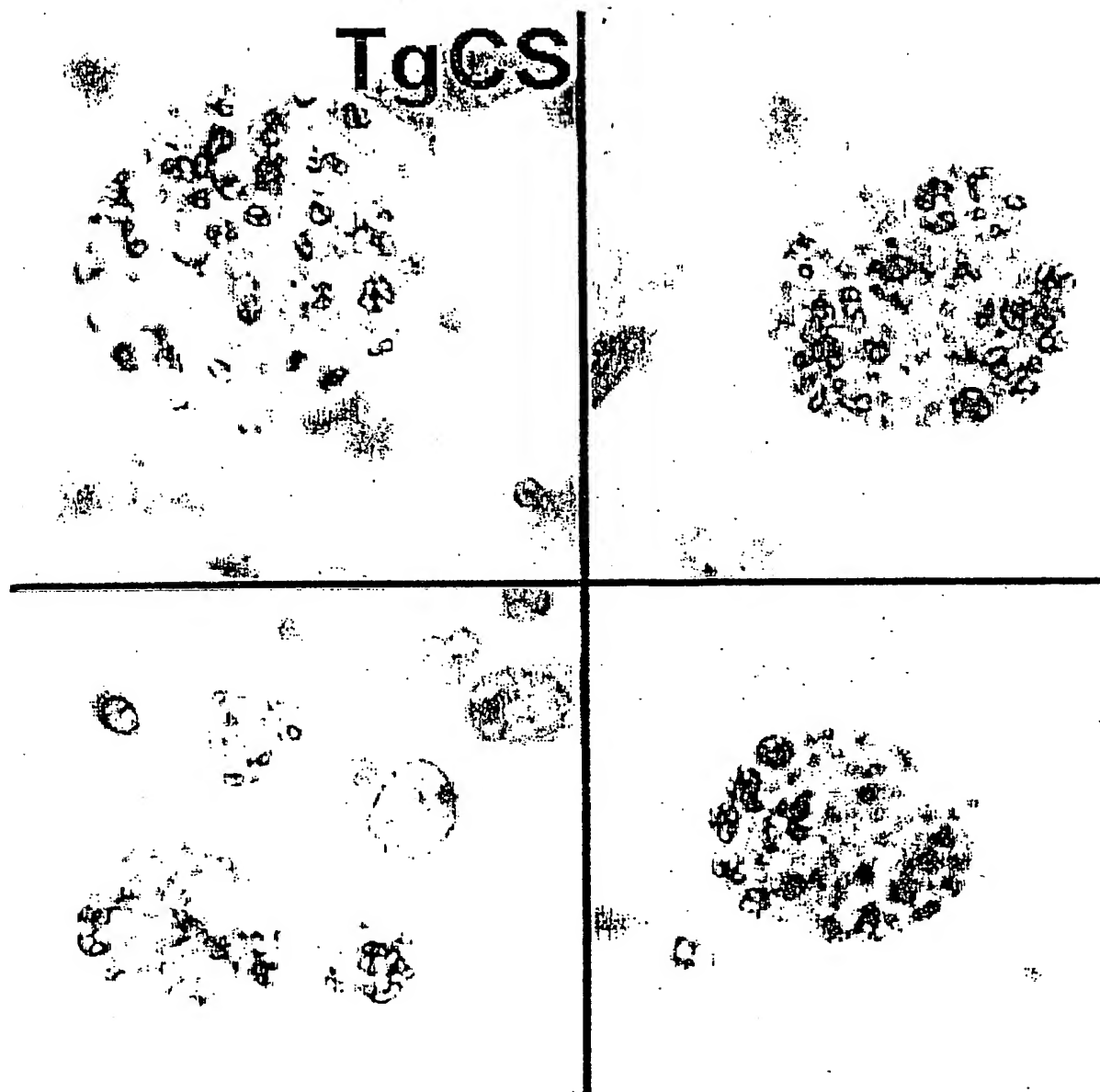


FIG 16C

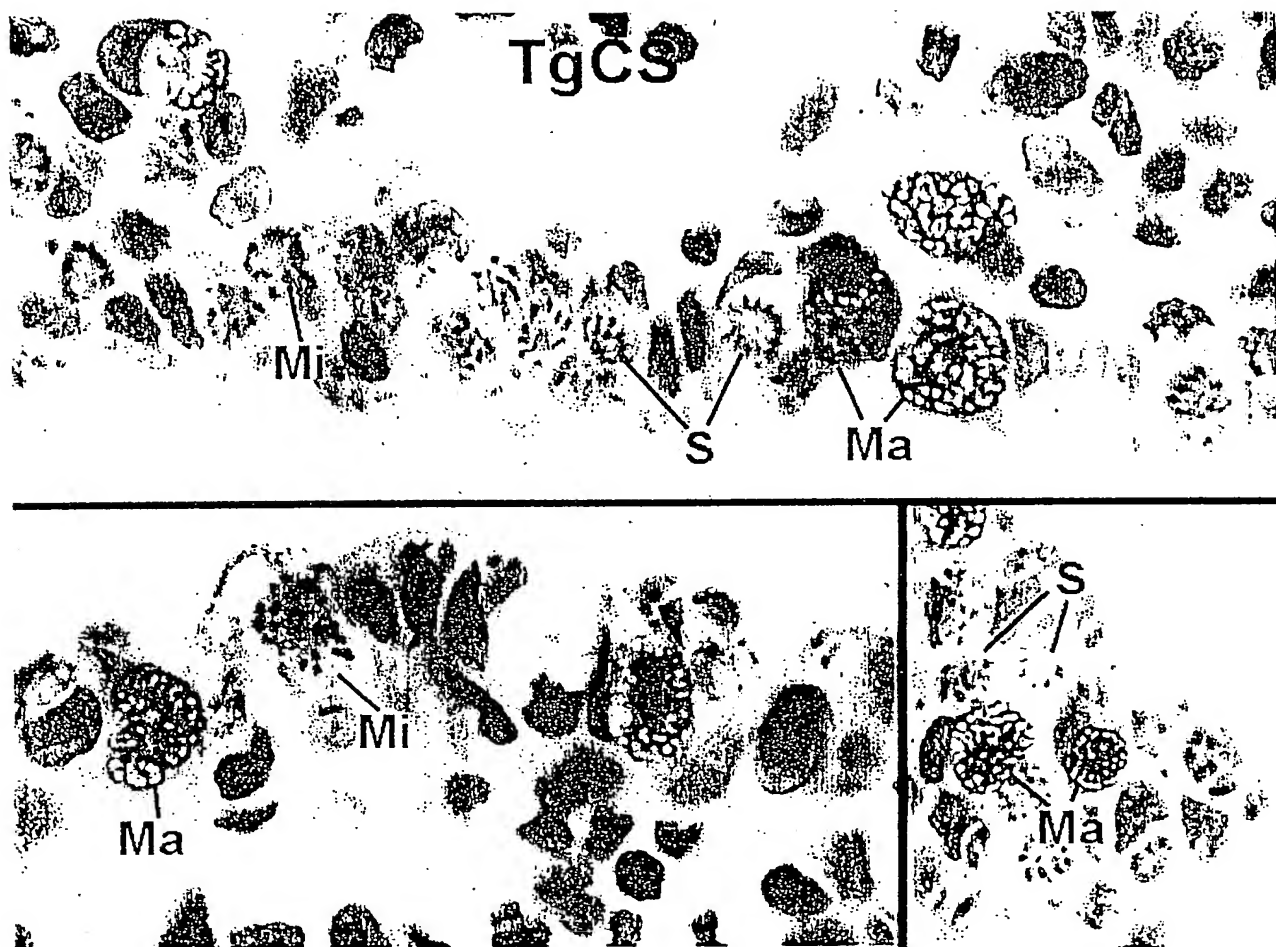


FIG. 16D

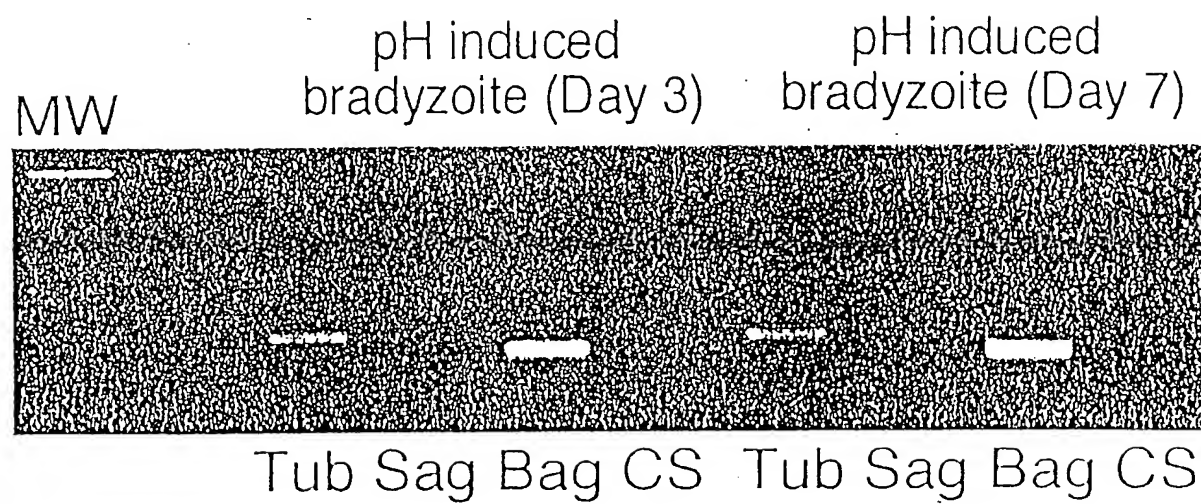
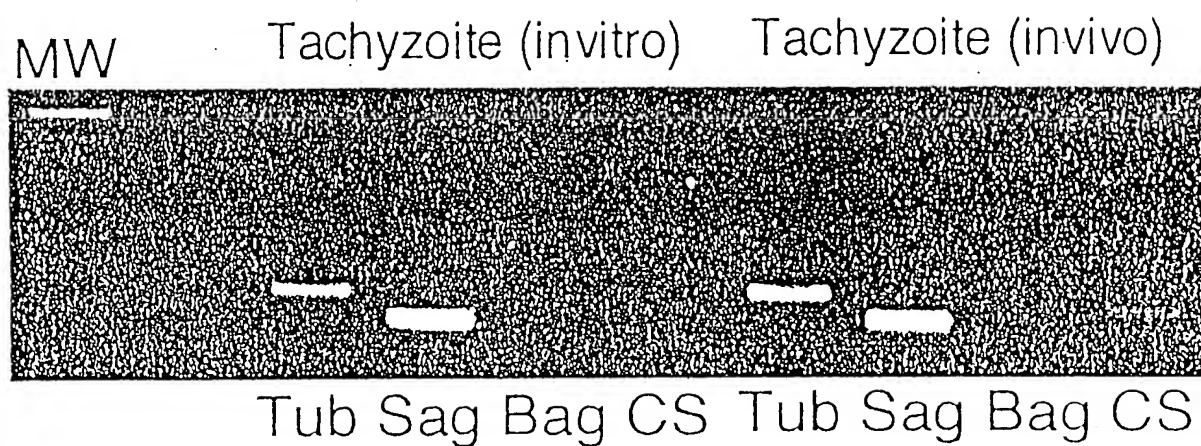


FIG. 17A

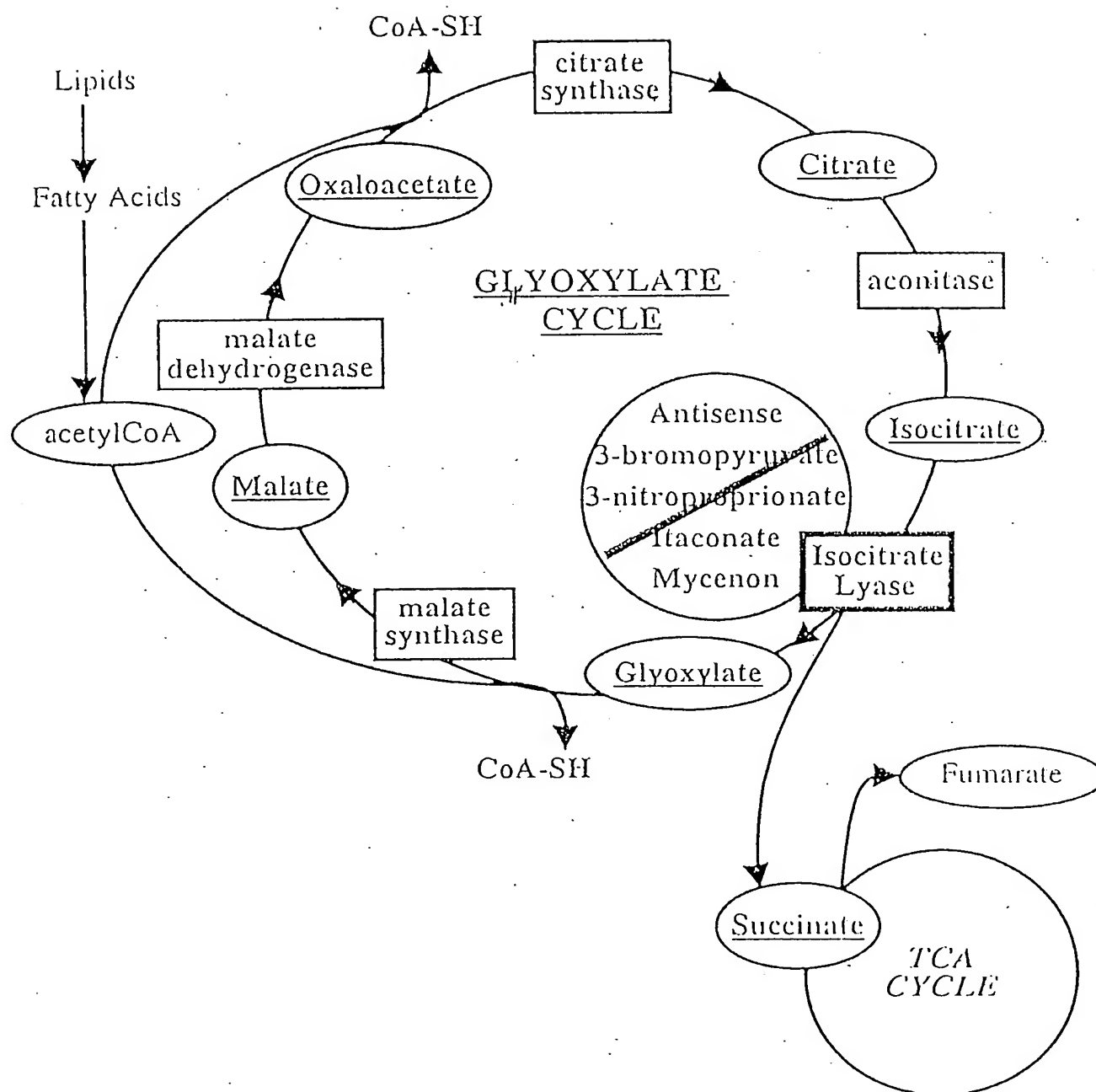


FIG. 17B

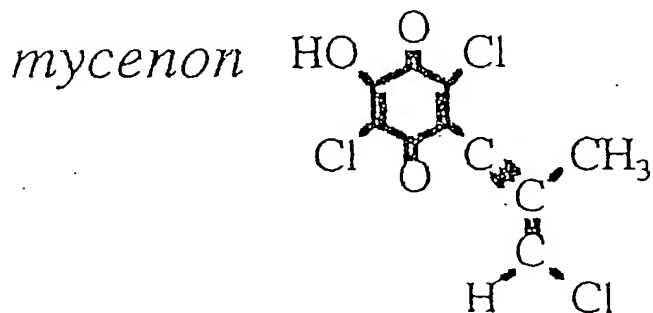
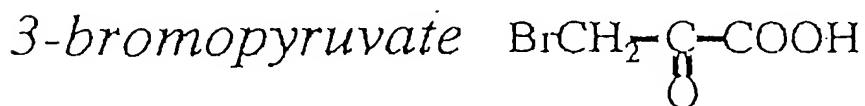
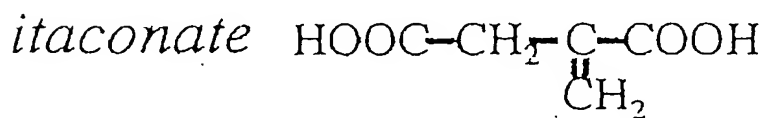
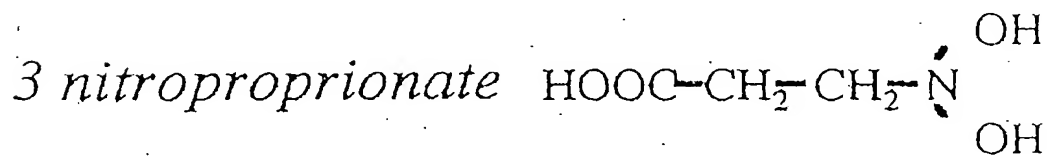
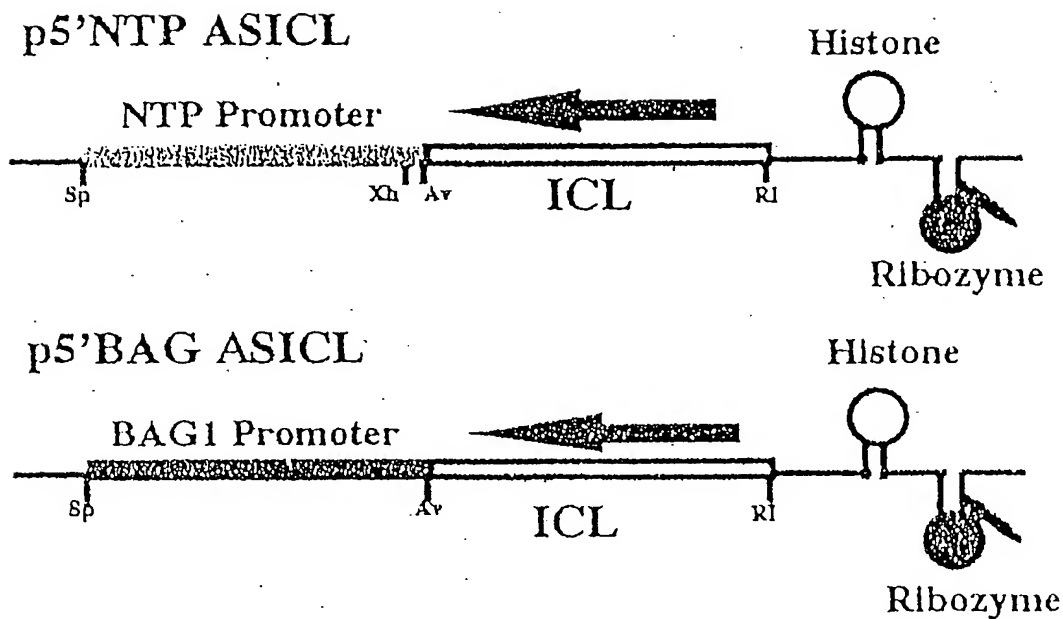


FIG. 17C

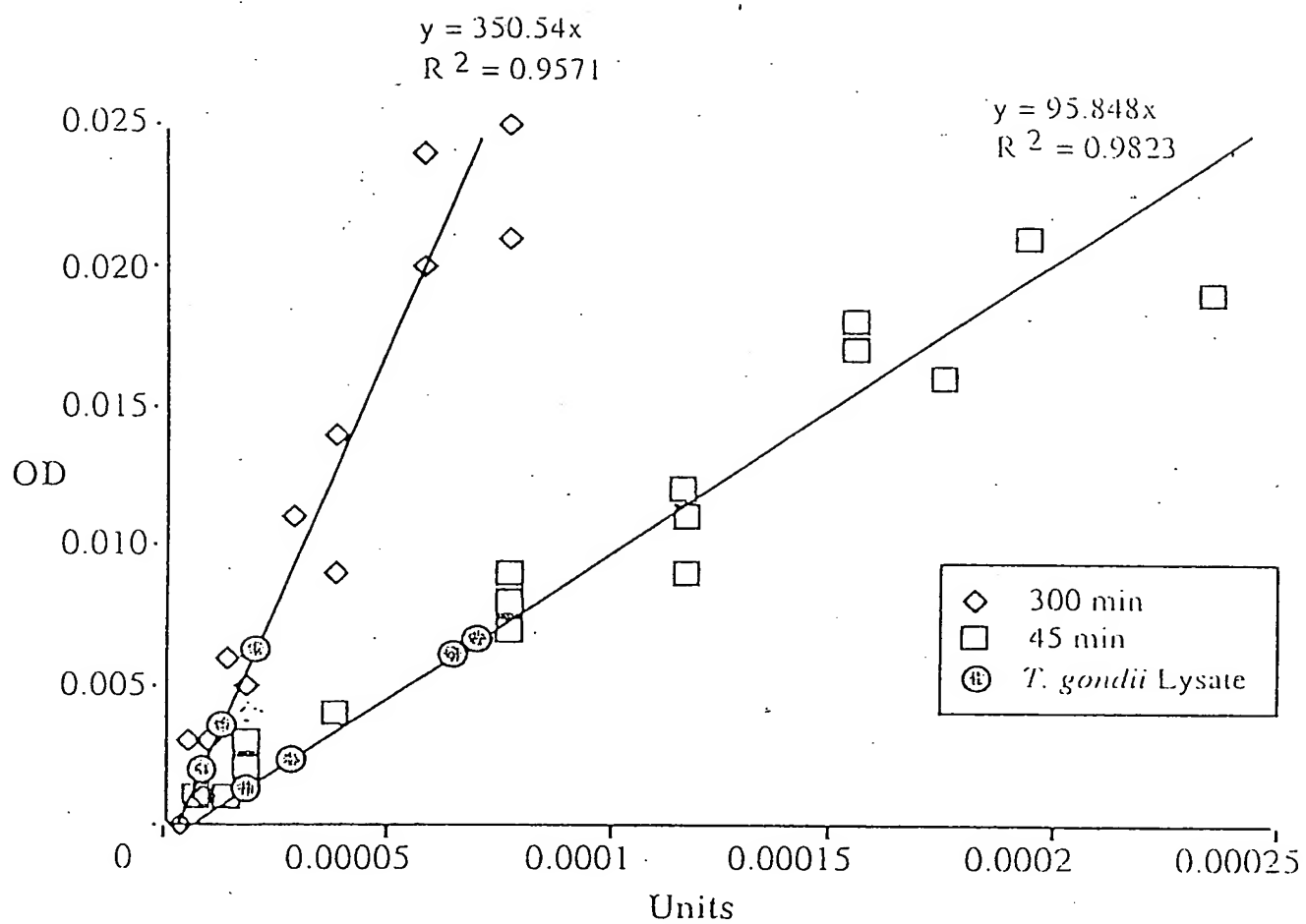
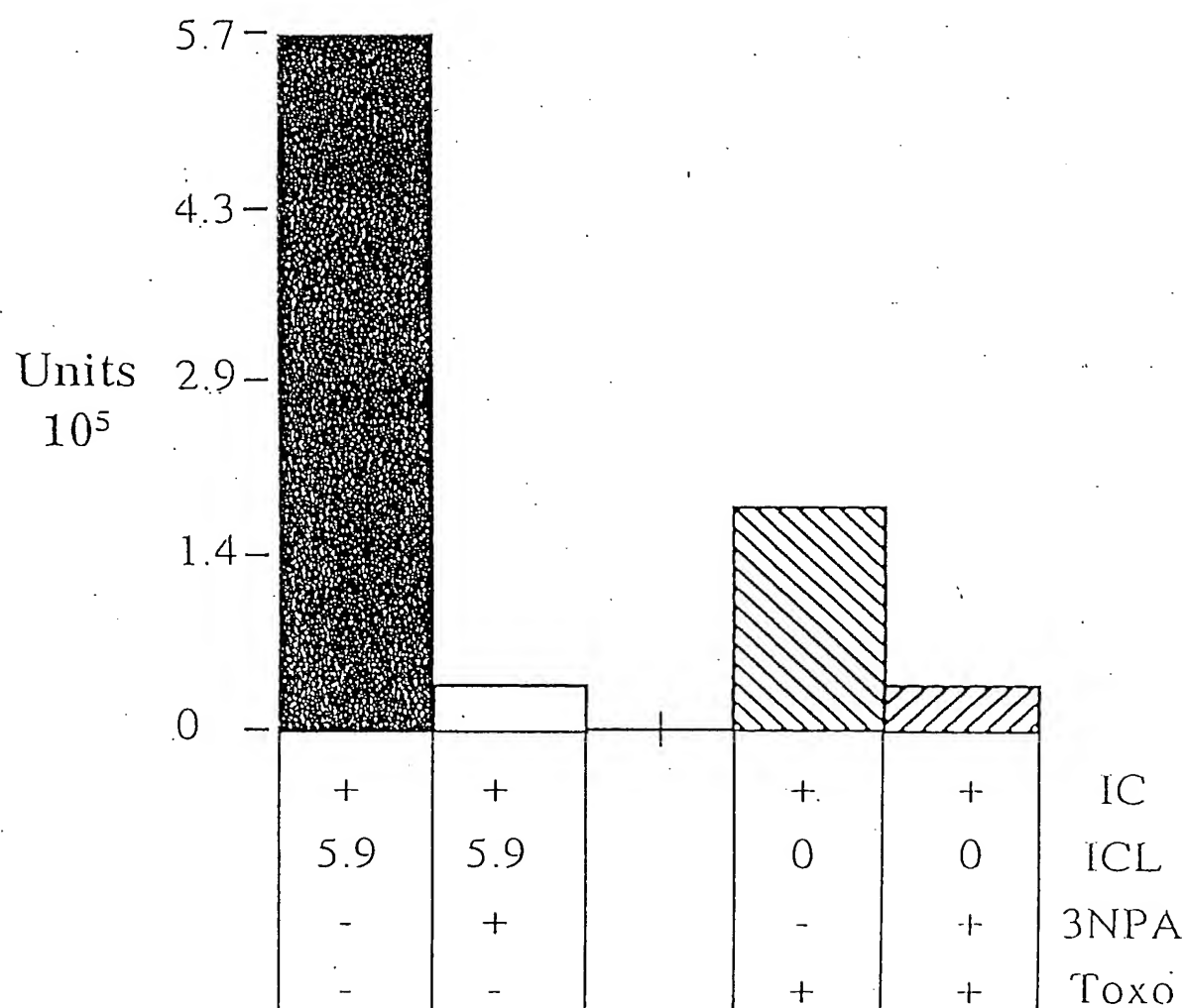


FIG. 17D



IC = Isocitrate [4mM]

ICL = Isocitrate Lyase [10^{-5} units]

3NPA = 3-nitropropionate [$1\mu\text{M}$]

Toxo = *T. gondii* Lysate

FIG. 17E

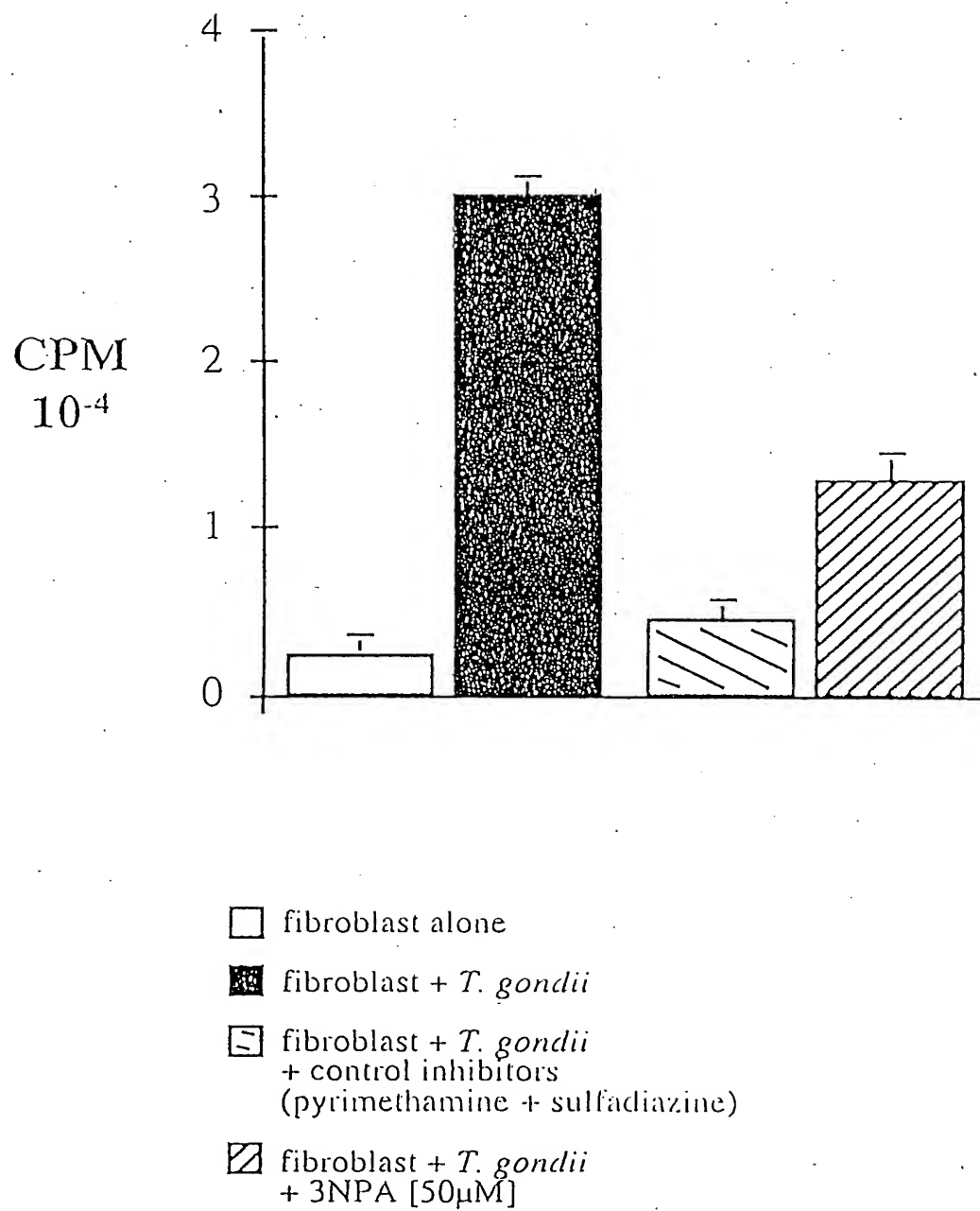


FIG. 18

AATACCCCTCCGAGTTCTATACGTTTCTTCGGTTTTTTGCTAAGCCACAAAC 50
 TGCAGGCTTAGCAGGCCACCTTCCGTCGTGAACCTCGTTCGCCGAGTTTACC 100
 GGCCTCACACCTATTTTCGTTGCCGTTCTGGAAAGTCAGTAAGGGACCAC 150
 CTTACGTCGAGTTGACCGGTCTGCAATGACCATTGAGTTTCGATGTCCTCG 200
 AAATCCTTTTGTTTTGATTTCCGCAAGGAGTGTCTTGAACCAC'TGTCGGT' 250
 GTCTACTTCCCTTTTTCGTCGCGCTTCCGCGCCGTCTCCCCGTCC'TCGTCT' 300
 CCGCCTTCCGTCTCACAAC'TTCCCTTCA'TTCTCACAGCATGGCGTCT'CCGT' 350
 GCTCCCCATGCTGGACAGCGCTTGCGCAGCCTCATGCAGAAGAAATGCGT' 400
 CATGCTTCCTGGGGCTTACAACGGTCTCACCGCGCGCCTCGCGGCTGAAG 450
 CAGGATTTGAAGGAGTCTACGTCTCTGGAGCTGCTCTCAGTGCATGCCAA 500
 GCGTCCCCGATATCGGCATATTAGGTCTCGAAGACTTTACTCGAGTAA'T 550
 CTCCCAAGCCGCCTCTGTCAACAGCCTCCCTG'TTCTCGCCGATGCAGACA 600
 CGGGGTTCGGTGGCCCTGAAATGGTTTCGGCGCACTGTCTTCGCGTACAAC 650
 CAGGCGGGCGCGGCTGGGCTGCACATTGAGGACCAGCGTTTGCCGAAGAA 700
 GTGCGGGCATTTGGAGGGGAAGCAGTTGGTGTCCATTGAAGAGATGGAGG 750
 AGAAAAATCAAAGCGGCCGCTGCGGCGTCCCAGGACTGCTCGAACGGCCGAC 800
 TTCATCATCTGCGCTCGCACGGACGCCCGCAGTGTGACGGGGCTTGA'TGC 850
 GGCTGTGGAGCGAGCAGTCCGATACACGGCAGCCGGAGCAGACATGCT'TT' 900
 TCCCCGAAGGACTGGAGACAGAGGTGAGAGGTGGAAAGAAGAATCAGAGG 950
 AAGAAGGCGTCTGTATTGGAGAGGCAGCGAGAGGCAGTCCG'TCTGGAAGA 1000
 GTTTCAAGCATTTGCGCATGCATTGGCGGTTTTTGCTTGGCAAAGCGCCT'T' 1050
 TCGGGGGGGCCCTATCTGCTCGCAAATATGACGGAATTTGGAAAGACGCCC 1100
 ATCATGGAGCTTTCCACCTTCGAAGGCCTTGGATACCACTGCGT'TATCTA 1150
 CCCTGTTTTACCTCTCAGAGTCGCCATGAAAAGCGTCAAGGGCATGCTGC 1200
 TCGACTTACGCAAGAA'TGGCAGCGTTGGCCATAGCCTGGAGAAAA'TGTAT' 1250
 ACACGGCAGGAGCTTTA'TTCCACTCTGCACTATCGGCCGGAAGGGACGTC 1300
 GACGTATCCC'TCAGCGAGTGTGTGCATGGACAAAGCCGTGGAAGATACCC 1350
 AGGCCTAGGGAGTCTCAGGCTCGGCATTTTCT'TTTTCTCGACTGGTCTCA 1400
 CCAATACAAAAGACAATGCTCACAGACGAAAAGCAGAAGT'TCTGAT'TGTA 1450
 T'TTATGAAACG'TGAAAAAATAAAAAAAAAAAC'TCGAGGGGGCGGCCGCTA 1499

FIG. 19

YPPSSIRFFGFC*ATNCRLSRPPSVVNSFAELPASHLFSLPFWKVSKEPP 50
SRAVDRSAMTIEFDVPKSFCFDFRKECLEPLSVSTSFFVALPRRLPVLS 100
AFRLTTSLSHSHSMASRAPHAGQRLRLSMQKKCVMLPGAYNGLTARLAAEA 150
GFECVYVSGAALSACQGVDPDIGILGLEDFTRVISQAASVTSLPVLADADT 200
GFGCPENVRRITVFAYNQACAAGLHIEDQRLPKKCGHLEGKQLVSIEMEE 250
KIKAAAAASQDCSNGDFIICARTDARSVDGLDAAVERAVRYTAAGADMIF 300
PEGLETEVRGGKKNQRKKASVLERQREAVALEEFQAFahalAVLPGKAPF 350
GGPYLLANMTEFGKTPIMELSTFEGLGyHCVIYPVSPLRVAMKSVKGMLV 400
DLRKNGSVGHSLEKMYTRQELYSTLHYRPEGTWYTPSASVCMDKAVEDTE 450
A*GVSGSAFSFSRLVSPIQKTMILTDEKQKF*LYL*NVKKKKKNSRGGPV 499

FIG. 20A (1)

		10	20	30		
B._napus	1:	MAASFSVP	SMIME	egRFEAPVAEVQ	TW: 28	
A._thalian	1:	MIDKPNQ	IME	egRFEAPVAEVQ	TW: 25	
R._communi	1:	MAASFSGP	SMIME	egRFEAPVAEVQ	AW: 28	
castor_bea	1:	MAASFSGP	SMIME	egRFEAPVAEVQ	AW: 28	
G._max	1:			EAAPVAEVQ	AW: 10	
Cucurbita	1:	MATSFSVP	SMIME	egRFEAPVAEVQ	AW: 28	
P._taeda	1:	MAIYSAQA	ENSILE	egRFEAPVSE	ETQAW: 29	
N._crassa	1:	MAANNMVNPA	VDPAL	DELFAKEVE	EVKKW: 30	
C._cinereu	1:		SSER	QAG	EVAVERN: 18	
E._coli.	1:			MKTRTQ	GLEE	LOKE: 14
T._gondii	1:	MTIEFDV		KSFC	DFRKEC	EP: 23
consensus	1:	-----*	-----*	*****	*****	-----*: 30

		40	50	60				
B._napus	29:	WSS	ERFELT	RPYTA	DVV	ALRGHL	KQGY	: 57
A._thalian	26:	WSS	ERFELT	RPYTA	DVV	ALRGHL	KQGY	: 54
R._communi	29:	WNS	ERFELT	RPYTA	DVV	ALRGHL	KQGY	: 57
castor_bea	29:	WNS	ERFELT	RPYTA	DVV	ALRGHL	KQGY	: 57
G._max	11:	WNS	ERFELT	RPYTA	DVV	SLRGHL	KQGY	: 39
Cucurbita	29:	WNS	ERFELT	RPYTA	DVV	SLRGHL	KQGY	: 57
P._taeda	30:	WNS	TQLE	RPYTA	DVV	RLRGHL	KQGY	: 59
N._crassa	31:	WSD	SRW	QTK	RPYTA	EQHV	SKRGHL	KIEY: 59
C._cinereu	19:	WKS	PRE	ARVN	RPYTA	ADV	SKRGHL	KINY: 47
E._coli.	15:	WTQ	PRW	EGIT	RPYTA	ADV	KLRGHL	SYNPEC: 43
T._gondii	24:	SV	STS	FVAL	PRRLPV	LVSAFR	LTTS	SLHS: 52
consensus	31:	*-*	*****	*****	*****	*****	*****	*****: 60

		70	80	90		
B._napus	58:	ASNem	AKKLWR	TK	HOVNGTASRTFCAL	: 86
A._thalian	55:	ASNem	AKKLWR	TK	HOANGTASRTFCAL	: 83
R._communi	58:	ASNem	AKKLWR	TK	HOANGTASRTFCAL	: 86
castor_bea	58:	ASNem	AKKLWR	TK	HOANGTASRTFCAL	: 86
G._max	40:	ASNem	AKKLWCL	LN	HOANGTASRTFCAL	: 68
Cucurbita	58:	ASNem	AKKLWR	TK	HOANGTASRTFCAL	: 86
P._taeda	60:	ASNem	AKKLWR	TK	HOANKTASRTFCAL	: 88
N._crassa	60:	ASNAQ	AKKLWR	ILE	DFAKRDASYTYGCL	: 88
C._cinereu	48:	PSAVQ	GKKLW	KL	SEHAKNGTSPSHTYGAL	: 76
E._coli.	44:	TLAQ	LGAKM	ARLL	HGESKKGYIN	: 72
T._gondii	53:	HMASRA	PHAGQR	LE	SLMQKKCVM	: 81
consensus	61:	*****	*****	*****	*****	*****: 90

— FROM FIG. 20A (1) —

FIG. 20A (2)

		100	110	120		
B._napus	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115
A._thalian	84:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:112
R._communi	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115
castor_bea	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115
G._max	69:	DPVQVT	QVAKH.	LD	TVVSGWQCSSTHT	St:97
Cucurbita	87:	DPVQVT	mVAKH.	LD	TVVSGWQCSSTHT	St:115
P._taeda	89:	DPVQVT	mVAKY.	LD	TVVSGWQCSSTHT	St:117
N._crassa	89:	QPTMVT	QVAKY.	LD	TVVSGWQSSSTAS	St:117
C._cinereu	77:	DPVQVT	KVAKY.	LD	TVVSGWQSSSTAS	St:105
E._coli.	73:	TG	QALQQA	KAG	EA	YVSGWQVADANLA:102
T._gondii	82:	ng	TAR	AAEAGF	EG	YVSG.....AALSA:106
consensus	91:	*****!*-*****!***:120				

		130	140	150		
B._napus	116:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:145
A._thalian	113:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:142
R._communi	116:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:145
castor_bea	116:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:145
G._max	98:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:127
Cucurbita	116:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:145
P._taeda	118:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:147
N._crassa	118:	NEEGPD	LADY	PYDTVP	PNKVEHLFFAQQY	HD:147
C._cinereu	106:	NEEGPD	LADY	PSN	TVPNKVEHLFFAQQY	HD:135
E._coli.	103:	ASMYPP	QEL	LYP	ANG	VEAVVEINNTFERRAD:132
T._gondii	107:	Cg	GV	ED	IG	ILGLDFT.....EV:124
consensus	121:	*****!!*****:150				

		160	170	180					
B._napus	146:	RKOR	BARMS	MSRBER	ATP	VDYL	IC	PTTAD	:175
A._thalian	143:	RKOR	BARMS	MSRBER	TIC	TP	VDYL	IC	PTTAD:172
R._communi	146:	RKOR	BARMS	MSRBER	ATP	VDYL	IC	PTTAD	:175
castor_bea	146:	RKOR	BARMS	MSRBER	ATP	VDYL	IC	PTTAD	:175
G._max	128:	RKOR	ERM	MSRBER	ATP	VDYL	IC	PTTAD	:157
Cucurbita	146:	RKOR	BARMS	MSRBER	ATP	VDYL	IC	PTTAD	:175
P._taeda	148:	RKOR	BARMS	MSRBER	STP	VDYL	IC	PTTAD	:177
N._crassa	148:	RKOR	QER	ISMP	QQR	ELAN	TDYL	IC	PTTAD:177
C._cinereu	136:	RKOR	EAR	SRMS	DAELAN	TEV	TDYL	IC	PTTAD:165
E._coli.	133:	QI	OWS	AC	LEPG	APR	Y	VDY	FLRIVAD:157
T._gondii	125:	IS	QAA	SVT	ST	BY	PTTAD	:139
consensus	151:	**!*****-*****!***!!:180							

FROM FIG. 20A (2)

FIG. 20A (3)

		190	200	210	
B._napus	176:	GGTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:205
A._thalian	173:	GDTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:202
R._communi	176:	GDTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:205
castor_bea	176:	GDTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:205
G._max	158:	GDTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:187
Cucurbita	176:	GDTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:205
P._taeda	178:	GDTCTGGG	TATVRLCKLFEVERGAAGVHT	AD	:207
N._crassa	178:	ADTCHGGL	TAVMKLTSLFEEKGAAGVHT	AD	:207
C._cinereu	166:	ADTCHGGL	TAVMKLTSLFEEKGAAGVHT	AD	:195
E._coli.	158:	AAACCTGG	VLNAFELMKAMTEAGAAVHT	AD	:187
T._gondii	140:	ADTCTGGG	PEMVRRTVFAYNQAGAAGVHT	AD	:169
consensus	181:	***!***	-*****	***!***!***!***!	:210

		220	230	240	
B._napus	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
A._thalian	203:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:232
R._communi	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
castor_bea	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
G._max	188:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:217
Cucurbita	206:	QS SVTKKCGHMAGKVLV	AVS	SEHINRLVAAR	:235
P._taeda	208:	QA SVTKKCGHMAGKVLV	SVG	SEHINRLVAAR	:237
N._crassa	208:	QAPGTTKCGHMAGKVLV	PTQ	SEHINRLVAAR	:237
C._cinereu	196:	QAPGTTKCGHMAGKVLV	PTQ	SEHINRLVAAR	:225
E._coli.	188:	QLASVTKKCGHMAGKVLV	PTQ	SEHINRLVAAR	:217
T._gondii	170:	Q.RIPKCGHMAGKVLV	SEH	SEHINRLVAAR	:198
consensus	211:	!-***!!!!!!*	***!***!***!***!	***!***!***!***!	:240

		250	260	270	
B._napus	236:	LQ . EDVNGTETV	LVARTDAVAPT	LTIQSNID	:264
A._thalian	233:	LQ . EDVNGTETV	LVARTDAVAPT	LTIQSNID	:261
R._communi	236:	LQ . EDVNGVETV	LVARTDAEAA	NLTIQSNID	:264
castor_bea	236:	LQ . EDVNGVETV	LVARTDAEAA	NLTIQSNID	:264
G._max	218:	LQ . EDVNGVETV	LVARTDAEAA	NLTIQSNID	:246
Cucurbita	236:	LQ . EDVNGVETV	LVARTDAVAPT	LTIQSNID	:264
P._taeda	238:	LQ . EDVNGVETV	LVARTDAVAPT	LTIQSNID	:266
N._crassa	238:	AO . ADVNGSGL	LVARTDAEAA	NLTIQSNID	:266
C._cinereu	226:	LQ . YDVGVENI	LVARTDAEAA	NLTIQSNID	:254
E._coli.	218:	LA . ADVTGVP	LVARTDAEAA	NLTIQSNID	:246
T._gondii	199:	AASQDCSNG	LVARTDAEAA	NLTIQSNID	:228
consensus	241:	*-***!***	***!***!***!***!	***!***!***!***!	:270

FIG. 20B

				210			220			230																			
gi	113033	Y	T	P	I	V	A	D	A	G	H	G	G	I	T	A	V	F	K	L	T	R	M	S	T	E	R	G	A
gi	113027	E	L	P	I	T	A	D	A	T	G	H	G	G	I	T	A	I	K	L	T	K	L	E	T	E	R	G	A
gi	2497268	Y	L	P	I	T	A	D	A	D	M	G	H	G	G	P	T	T	V	M	K	V	A	K	L	T	A	K	G
consensus		*	!	*	!	!	*	!	!	!	!	!	!	!	-	!	!	!	!	*	!	*	*	*	!	*	*	!	*

. . . 240 . . . 250 . . . 260 . . . 270
 A G T T m m D Q T S T N K K C G H M A G L C M I P V Q E E V N R L V T I R M C A
 A G T T I T D Q A P G T K K C G H M A G L V L V P V Q E E H N R L V A I R A S A
 A G T T I T D Q M V G G K K C G H L S C A V L V E T A T H I M R L I S T R F Q W
 ! ! ! ! * ! ! ! - - * - ! * ! ! ! * * ! * * * * ! * * * ! * * ! ! * * * ! - - *

. . . 280 . . . 290 . . . 300
 DBMHSdLIVVARDSSEATTSSTTDTRD:271
 DIEGSNLLAVARDSSEATTESTTDHRD:264
 DIMGUeNLVIARDS CNGKLLSSSDPRD:292
 ! ! * * * * * * * * ! ! ! ! ! * * * * ! * * ! * * ! - ! ! :300

FIG. 21(1)

CCCTATTACGTTTCCTTTTTTTAAATGCGGCGAAAACATTCCCTCCATAC	050
AGATTTCCCATTCACGTGACGTCTCGCGTGTTCAAACGTCAACTGGTTT	100
TCCCTGCTCTTGTAGTCACAAGACCGTGCAACCAAACCTGCGACACAATC	150
TTGTGCCGTGTGACCACCGCACCGCAACTGCCCACTCTGTAAACATAGTCC	200
CTCCCTAAACCGTCAAAACCCCGAAACGAACCGGATGCTCTTCTCTCGTC	250
CTTTCTCCCTCGTTTTCTTTCTTAGAAAAACAGGAAAAATCCTCACTGGA	300
TATGTGCACATTTACCGAAGCGATGCGGAATCCACGGCGAGGTGGCGGGT	350
CAACTCCCTTGGCCAGGGGTGAGTCTGGTAGTGCCATTTTAGGCGTAG	400
AGACAAATGTAAAGGTCTCCCATTTGAACAGAACCTGCTTACTCCTTCGTCT	450
TAGCCCCCTCAATTCTGCATTTACAATCCCTTTCAAAAGCAACAAAGTCTT	500
ACATCCAAAACCCCTCCAAAATCCCGTGGTGTGTGACCTTTCCAGTGACTC	550
TTGCTCCCACAACCGTGCGCCCTTTTCGCGGCTTGCCGAAACATCGAAA	600
AGCTGCGTCGCTCGCATTACTGCTTTTTGGGCCTTCACTTTTCCCCAAAT	650
ACCCTCCGAGTTCTATACGTTTCTTCGGTTTTTGCTAAGCCACAAACTGC	700
AGGCTTAGCAGGCCACCTTCCGTCGTGAACCTCGTTCACCGAGTTACCGGC	750
CTCACACCTATTTTCGTTGCCGTCTGGAAGTCAGTAAGGGACCACCTT	800
CACGTGCAGTTGACCGGTCTGCAATGACCATTGAGTTCGATGTCCCGAAA	850
TCCTTTTGTGTTTGATTTCCGCAAGGAGTGTCTTGAACCACTGTCCGTGTC	900
TACTTCCTTTTTCGTGCGCCTTCCGCGCCGTCTCCCCGTCTCTCGTCTCGG	950
CCTTCCGTCTCACAACCTTCCCTTCATTCTCACAGGTGGTGTACTGCAATC	1000
ATAAAGAACTTGCTGTCTGCACCTCTTATGCAGAGTCATATTCAGTCTC	1050
CTACGGAATATCATGTCCACAAATAAAGAAAACCTGGTTTGATTGTATCTC	1100
ATCACTGACTGTCTCGTCCGACCCTTCCCCCCCCATAAAATAGCTGCTAACG	1150
TGCAATGATTGAGATACATTTATCTACCGCACTTTAGTTTAATACCCCG	1200
GTTTGTGGTTAGGGTTGTATGAACGCAGGAATACTTGTAGATCTTTGGAG	1250
CTTAAATATAAAAGATGCATGTTTATATGTGAATCTTTCAATGAAAAAT	1300
GTACGTGCATCTACACGTCTTGAAACGTAGGTGTACAACAATGTGCTTGG	1350
GAAGTCACTGCCTCTCTACAAATCACATAGTTTCTGTACGGTGGCGCCTC	1400
ATTTTCTTTCTTTGACTCTCTGTTTGGCGTGTCAACATGATCTACCCTCGA	1450
TCC'TCCCAACAGTCCTTTTCGCTGTGCTTATCACTCTTTTTCTTTCAGTCC	1500
TTTCTTGCTGTGCTCGTCCGAATTGCCTATTTCTCTCCACTCTTTCTCTT	1550
CTTCTTCCCTGACGTGGTCTTGTGCGGTTGTCCGGGTTTCCCTCTGTCA	1600
T'TTCTTAACCGCTGCCTTCCCTCTCCTGTTGCTGCAGCATGGCGTCTCG	1650
TGCTCCCCATGCTGGACAGCGCTT'GCGCAGCCTCA'GCAGAAGAAATGCG	1700
TCATGCTTCCCTGGGGCTTACAACGGTCTCACCGCGCGCCTCGCGGCTGAA	1750
GCAGGATTTGAAGGAGTCTACGTCTCTGGAGCTGCTCTCAGTGCATGCCA	1800
AGGCGTCCCCGATATCGGCATATTAGGTCTCGAAGACTTTACTCGAGTAA	1850
TCTCCCAAGCCGCCTCTGTCAACAGCCTCCCTGTTCTCGCCGGTGCCTAG	1900
CAGAATCGTGTTCTTCACTTCTTACTTCTATCTGCTTTGTGTCTTTCTTG	1950
TTTTTGGTTTCGACTTGCTTGTGCTGATGGATAGAACCCACGTTGGGTGTT	2000
CGACGCGCCTCGAGCTTCTTCACTTGCCTACCTTCTGTACTCTTCTCTGA	2050
CTTTCGCTTCCCTAGTCTCGAGGATCCACGTGCTTTTCGACTCGTCCCTTG	2100
TCGCCGTATCGCTTCAGAAACCGTTCACATCTACTGGCCCTTCCCTCGTC	2150
TTTTCTTTTCCCTCGATGTCCTTTTCCCAACTTTTCGCTCTGCTCTCTCTC	2200

— FROM FIG. 21(1) —

FIG. 21(2)

TCCTCTGTCGACGGTCTGGTCACTCATTTCGTTTCGTGTCGCGTTCCCGTT	2250
GTGCTCTTTTCTCTCTTCTTCTCGTCCCTCTCCGTCTTCTCGCTCTCCTG	2300
TTCTCCTACCCGCTCTCCTTTTCTGTCTCGTCCGCTCAACCTCTCTCTCT	2350
TTTCCGAGCTCTTGCTTAGATGCAGACACGGGGTTCGGTGGCCCTGAAAT	2400
GGTTCGGCGCACTGTCTTCGCGTACAACCAGGCGGGCGCGGCTGGGCTGC	2450
ACATTGAGGACCAGCGTTTGGCGAAGAAGTGCGGGCATTTGGAGGGGAAG	2500
CAGTTGGTGTCCATTGAAGAGATGGAGGAGAAAATCAAAGCGGCCGCTGC	2550
GGCGTCCCAGGACTGCTCGAACGGCGACTTCATCATCTGCGCTCGCACGG	2600
ACGCCCCGAGTGTCGACGGTGGGTGACCCTCGAAACGGCCGAAAACAGAA	2650
CTCTAGGGTCTCGCGCATTACAGCGCGGGTGTCCCTCGAATGGACGCTAC	2700
AGTGCTGTTAGTGTCGAGTGTCTTTTAGCGACTTTCTTCAGAGCTCACTTA	2750
GGTTTCGTACGATTTCAATCGACAGACGGAAAGACGCTCAAGTGAAATTC	2800
GGGCCACCGAGAAGGCGAAGAGAGAGCAGAGGAAGGGAGGACCGGGAACC	2850
TTTGGACTACTGAGAAGCAGGCGAAGACGGGCGTTTCAGAAGCGCCTGAG	2900
CAGGTCTCCACACCGAGAGAAGCAGACTGAAGACGCAGTTCAGATGAAGC	2950
TGAAAACCGGAAAGCGCCTCTTTAATATTGTAGAGGGAGTCTTAAGTCG	3000
TGCCCTCTTTTCTCCCTGTCTTTCTCGCTGTCTCTGCAFGGCTCAGGGCTT	3050
GATGCGGCTGTGGAGCGAGCAGTCCGATACACGGCAGCCGGAGCAGACAT	3100
GCTTTTCCCCGAAGGACTGGAGACAGAGGTGAGAGGTGGAAAGAAGAATC	3150
AGAGGAAGAAGGCGTCGTATTGGAGAGGCAGCGAGAGGCAGTCGCTCTGG	3200
TGAGAAGCTGCGGCGGAAAGGGAGAAAGAAAGAAATGAAAAACCCGGT	3250
CGAGAGGGATGGAACCTGAAAACCTCGGAGAAGTGGAGAAAGGGAGCTAG	3300
GAGCAGAGGAGGTGAAGGAATCCGTATAGTGGATTGATGTGTGACGTCAA	3350
CTATGAAAGACATGACAAATTCAACTACAGGCGAAGGGTATGACAGGGAC	3400
ATGCGTTTTGTACAGAAAACAGAGGACAATGAACATGTCAGACCTCATA	3450
CACACGCGAAGAGATGCGCAGTGGATTATGGAATGAGCAAGAGTAAGGAG	3500
TGAAACTTCACAATGTGCATTTCGGTGTGAGTTGAGTCATCAAATCTCGG	3550
TGTTTCGTGCTCTTTTTTCTCGTCTGCCTCCAAAAGTGTGTCTTGCCTTC	3600
CTCATGCTGCTCTGCACCCATTGTCCTTACCCTGTTCCGTTTCGCTCCC	3650
CGTATGCCTGCGGTTTCTTGTCCGTTATCAGTCTCTACCGGGTTCATCTC	3700
CTCTTTCTGCGGAGAGGCTTTTGTCTAGCGATGGGTGTATGAGTTCTGT	3750
TCTGTCTATCCTCATATACCTACCGTCACGAGACAAACAACCTGCTCCATGGT	3800
CGCTGTACACGGCCAACCTTGTGGGCTGCTCACAAAAGCCACAAGTGTCTG	3850
AGTTTCAAAAATTCAACCACATTAGTGTGTGTTCCACGTCGGTTACGTTTAC	3900
GCGTTTCGCGAAGAAGACGAAGACGAAAGACGCGTCCATTTCAGAGAAGA	3950
CCTGTCCGTTTTTCGTTGTGACACCAGGAAGAGTTTCAAGCATTTCGCAAT	4000
GCATTGGCGGTTTTTCCTGGCAAAGCGCCTTTCGGGGGGCCCTATCTGCT	4050
CGAAAATATGACGGAATTTGGAAAGACGCCCATCATGGAGCTTTCACCTT	4100
TCGAAGGCCTTGGATACCACTGCGTTATCTACCCTGTTTCACCTCTCAGA	4150
GTCGCCATGAAAAGCGTCAAGGTACGTTTGTCTGCTATCCATACTGAGT	4200
GACTCGGATCGATTTCTTCGTTTGTGTGGCACGTGGAACCTGAGTGCCAT	4250
ATGCGTGTACGCAATGCAGAGGAATGCATGCATGTGAGCACACCTGTCT	4300
GCAGCTACGCGAATCTCTGCCTGTGTTGACCTTCTACCTGATGGCAGGCA	4350
TGCACGTGTATACACGCACAAGCATCTGTATAAATATGTGTAGTTGAGTA	4400

— FROM FIG. 21(2) —

FIG. 21(3)

ATTATACGTGACCTATTAAATCTAAAGCAGAAAACATGCTCATACCGTTC	4450
TTGTGTGTGCTCAGGGCATGCTGGTCGACTTACGCAAGAATGGCAGCGTT	4500
GGCCATAGCCTGGAGAAAATGTATACACGGCAGGTACAGCGTTACCATCA	4550
TAAGGCGGATACTTATAAGATTTTCCTTCAATGACGTGCATGCATCACGG	4600
ATACCAAACCTGCTCGTTTAATCCTCTGTTTTGCTCTGTAAGCGTCTTCC	4650
TTCTTGTAATTCTTCCATCCTTTTCATCTGCCGTTGTGTCAATTTCTGCCCT	4700
GGGGCTCTGTCTTCGCTTTAATGCCCTCAGTGTTTTCTTCTTTCTTGCC	4750
TCTCCTTATTCTGTCTCACGGTTCCTGTTTGTCTTCTGGTATCTCGTGCT	4800
GTTGCTGCTTTTAGGAGCTTTATTCCACTCTGCACTATCGGCCGGAAGGG	4850
ACGTGGACGTATCCCTCAGCGAGTGTTGTGCATGGACAAAGCCGTGGAAGA	4900
TACCGAGGCCTAGGGAGTCTCAGGCTCGGCATTTTCTTTTCTCGACTGG	4950
TCTCACCAATACAAAAGACAATGCTCACAGACGAAAAGCAGAAGTTCTGA	5000
AAAGACAAAAGGACGAAAGCGAGGAAACATGGCACACGACGGCGGGGGGA	5050
CTCTCAC'TGCACAACGTTATTCCAACCAAGTGCAAGAGTACCCGGATGT	5100
CCTTTGGTGTATGAATGCATGGTCTTTTTCAATTCCATCTGGCTGCTTCC	5150
GTGAAATTTTCGACGAGAAGCAAGAACAGAAGGCGAGCTTTTGTCACTGCG	5200
GCTAGTCGCCAATATTGAAGGGCCCGGGGGGGGGGAGCAACACAAACC	5250
ACAGAAAAGGAAGGCGTCTGCAAAATTTGCGGCGTCCCTCTTGGAAGAA	5300
AGAAAACCGAAGAGGATGGACAACTTACCCACCGAGGACAGACCACAGA	5350
TGCGAAAAAGAGAATGAATCGAGAGAAAAGAAATGCGAGCCGATGCAGAG	5400
GGGTCTCTTTCGTTTGAGGAGTTTCCAGGAGGGAAGCGAAAGAGACGTTT	5450
GGAAACCGGAAAGTGGACAAAACCTCCTTAAATGCGGAAGAGTGAGGCG	5500
AATGCAGGGCGGCTGTCTGTTTCTCTTACGAACTGTTCAAGGGTTAGA	5550
AACCCAGTAGAGTGCTCGTGACATCTTCCACTTTTCGTGTCTCACTTGGG	5600
TGCTCGGTTTCTGCAGTGCAAGCTGCTTCTCGCTGTCTCACTTCTTCT	5650
ATTGAGTAGACGAGGCACAGCGACCGGTTCTGCTGCGCGTTGTGTGAA	5700
AGGGGAAC'TCTGAGAGGCGTTTGTCTTTATGTTTTCTAACTGGTAGAGAG	5750
GGACGTGGTAGCGTGAAAAAACCGGCGTTTCTTTTGTCTCACGGCAGCAC	5800
ATGAGAAAGCTTCGGAGGTAGATGTGTTTTCGTCTAAATGCATTTCTCG	5850
GAAAAGAACGCCAGAGAACGGTAAATTCCTAGACAGTGACTGAGAGTGG	5900
ACTCGCACT'ACCCTCCGCCGCGACTGCGTCTTTTCTCCACTCTGCGAA'	5950
CTCACTTTTCTTCTGAATTTCTTTGTGCGACGAGGAACCGCGGTAGAC	6000
GGCGGCACAGCGTTTCTAGCAGATATTCCGGTTTGTGTGATTAGTGTCT	6050
GTCTCTTTCTCTCACTCTCACTTCTTGCCCGGAAGGAGGAACGCCGCAG	6100
AAAAGCAAAAACACCGGCGAGTGGAACCCAGTTTTCGGTAGCTTCAGCTGA	6150
GGCCCGCCGGTCGCGAGCGAAACTTCTCGGATTTATCCTCCAGCACTGAC	6200
AAAACCCTCTGGTGCAGATACGCAAAATGCGCATGCACGTGGAAGACGTCA	6250
AAGATATCCTTGCGATGAGCACGCAAAAGAGCCTGGAACGCATGCGCTAG	6300
AAACCCGCGAAGCACCCCAAAGTCGGCAATCTCTGTCTCACGTGCACACC	6350
ACCGCGATGACCACGGGAAACGGGACAGACTCTACAAACCTCCAAAATCT	6400
CTGTCCGACACCAAAAAACAAACACGGATTCCTGACGACAAAAAGACTC	6450
TCAACATCACATCCATGTGTGCATCTCTCTACACACTTGTGGCGGAA'AC	6500
ACATTTGTATCCATACATATACTTTCTAGTCGCGCTGCAGAGAGCTCCG'	6550
CGGTGTTCTTCTTCTGATCGGAATGGCTCGCTAGCGAGAGTCTTTGCCA	6600

— FROM FIG. 21(3) —

FIG. 21(4)

TTTCGCCACTTTTCCCTCTCTAGTTCAAGGTCTGAAAAAGACCATTTACG	6650
TTTTGAACTCTGCTCTGTCTCTCGGATCGCTCATCTGCTTTCCAGCTCCC	6700
TCTCTCCGCACATAAGCCGAATGTCATTCTCTCCTCTCAGTCTGCCC'TTG	6750
CCCGGCTTCCCAGACGAGGGGTTTTACGAAAAAATGCCGCCTCACCGTCA	6800
GAGCATTTGCTCCACACCTTCTTCCGCTGGCTTTCCCCTCTGCTTCTCC	6850
GTGTTTCTCTTGATTCACTTTTGCCTTCTCTCTTGTCTCCGCCCCGTCTG	6900
CGCGACCGCTTCAATCTAGGAGAGGCACACTCCCCCGAAAGAGCGTGTT	6950
GCTTTGCGCCTTCTCCTTCTAACTCGCTTTCCCCACAGGAGGCAGTTAAG	7000
AAGAATCTCAAAAGGATCCCAGAAGACACCCTTAGAAATCTCGAAAAAAC	7050
GCTCAAGAACCTCAGAAGAATCTCTCGGAAACCTCAGCAGAACCCGTCAT	7100
GGAGCTCTCAGAAGTTTCTTCAGAATCTCTCTAGAGGAGA	7141

FIG. 22

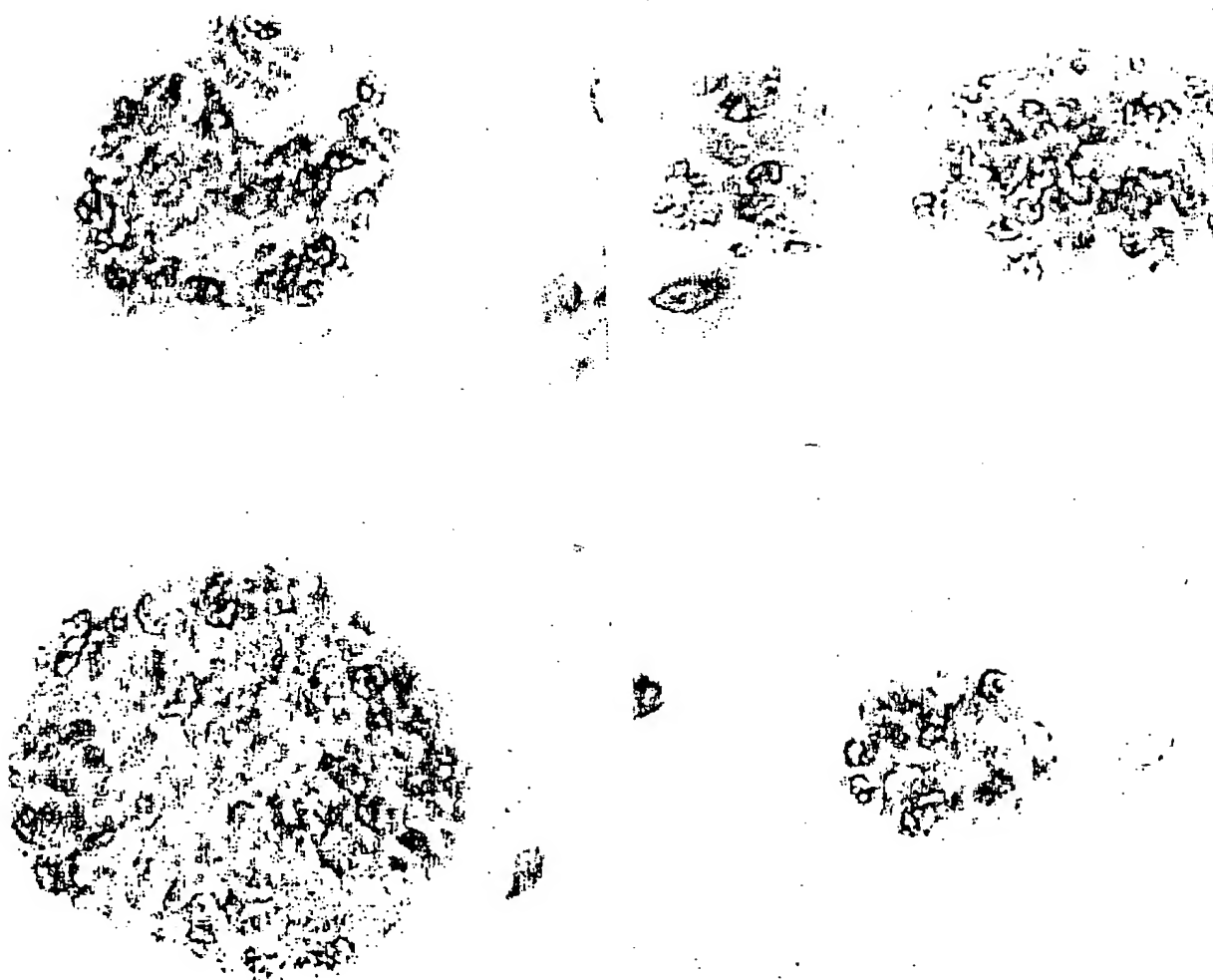


FIG. 23A KEY

- 1 = Cotton lysate + rabbit anti-ICL
- 2 = *T. gondii* lysate + rabbit anti-ICL
- 3 = Cotton lysate + rabbit anti-MS
- 4 = *T. gondii* lysate + rabbit anti-MS
- 5 = Cotton lysate + rabbit pre-immune
- 6 = *T. gondii* lysate + rabbit pre-immune

➡ indicates ~ 60 kd proteins reactive with anti-cotton isocitrate lysate (ICL) or anti-cotton malate synthase (MS).

⬅ indicates *T. gondii* protein reactive with anti-cotton MS.

FIG. 23A

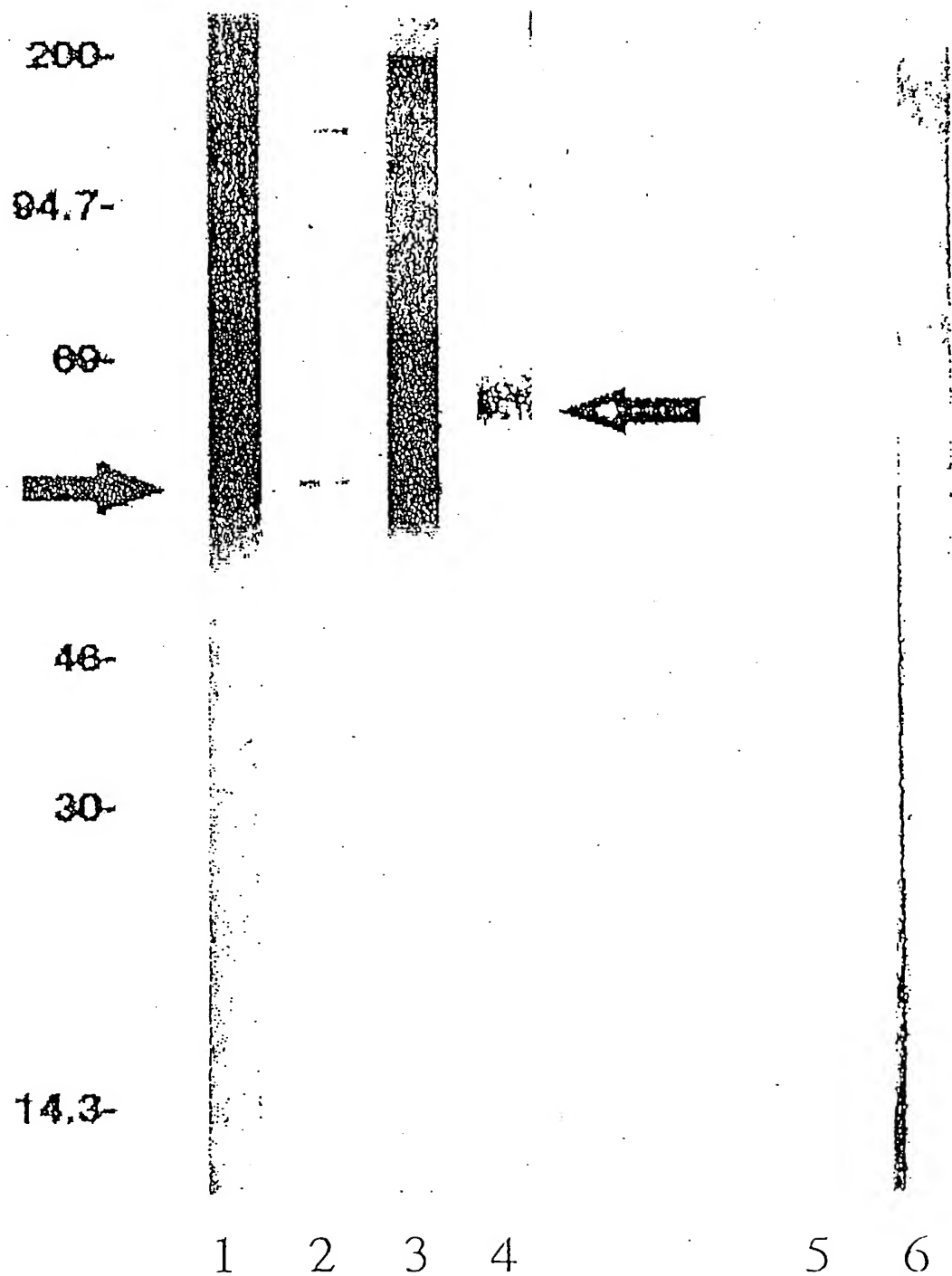


FIG. 23B

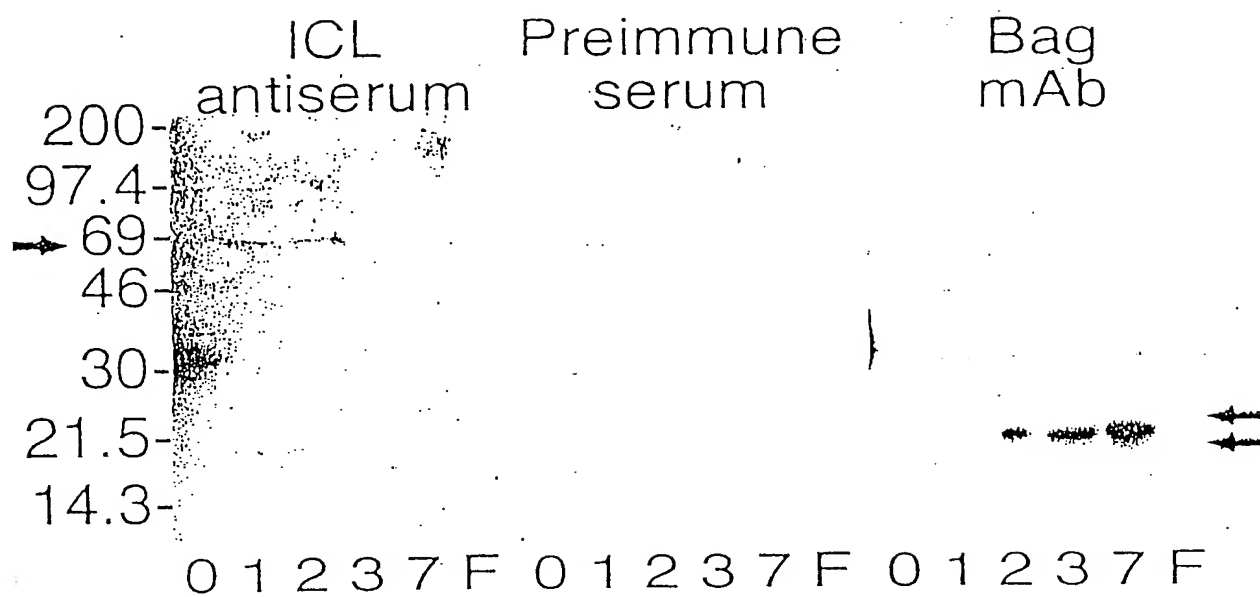


FIG. 23C

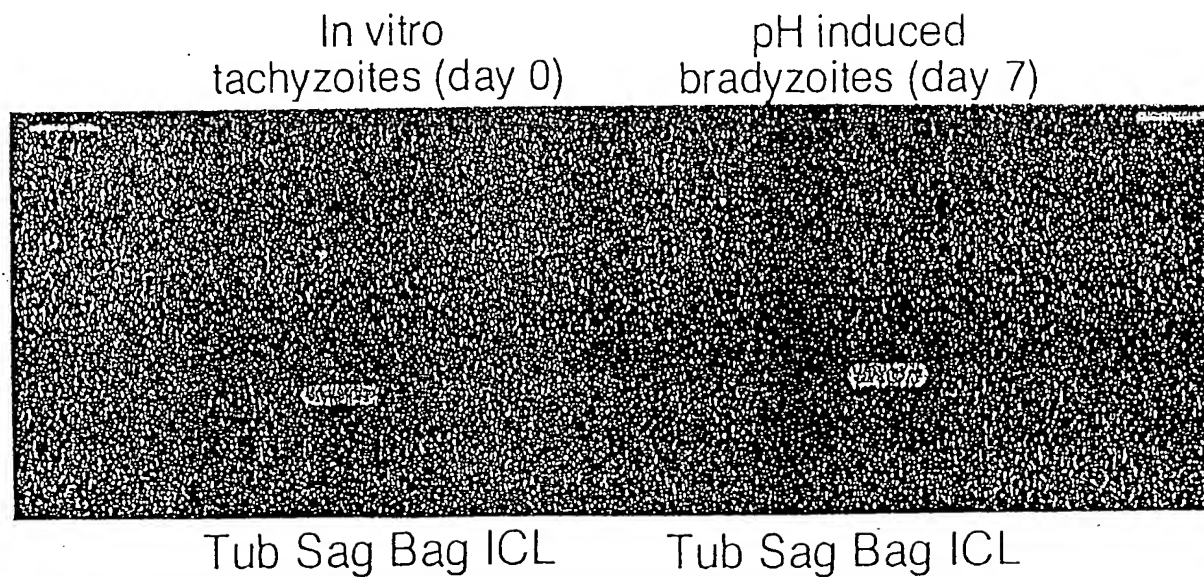


FIG. 24A

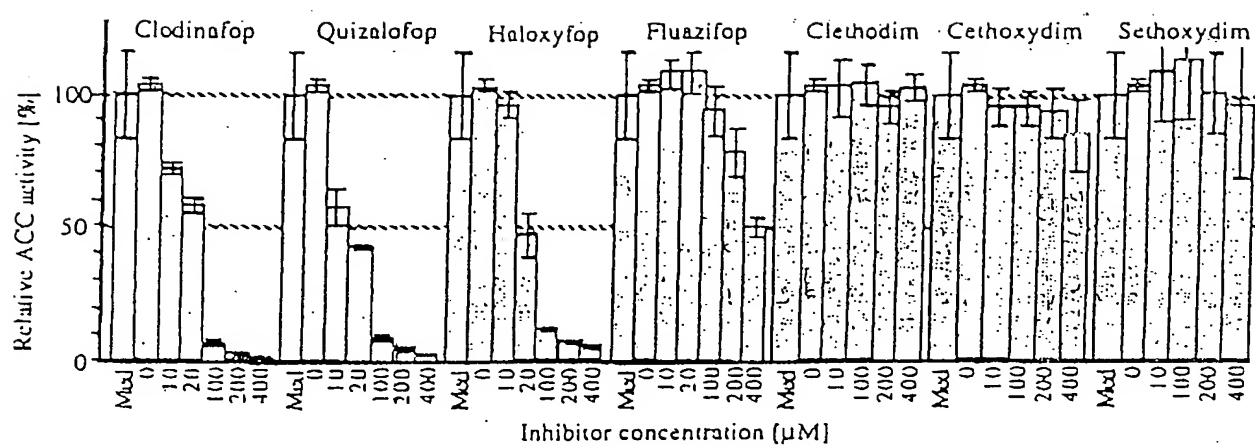


FIG. 24B

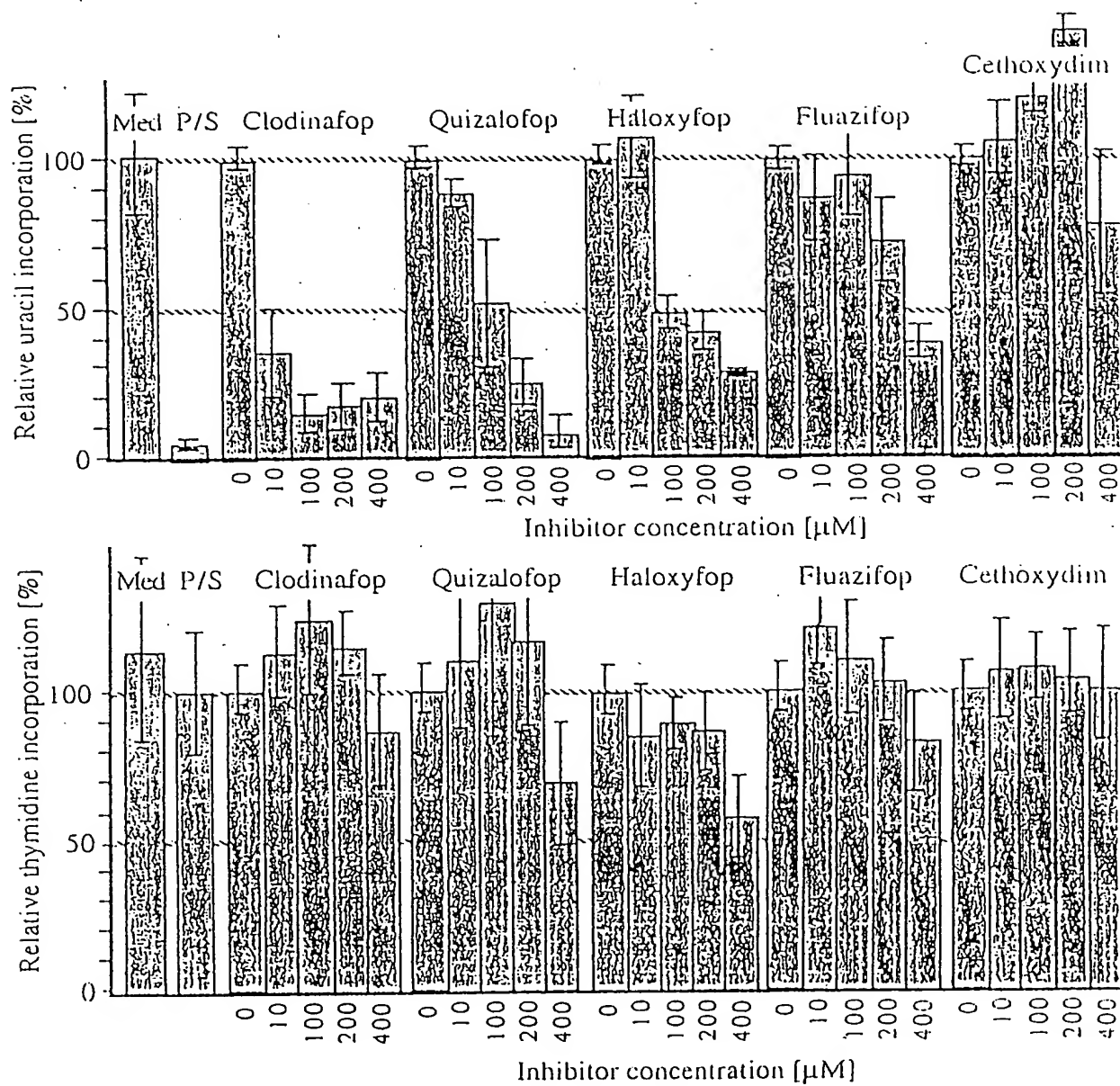


FIG. 24C

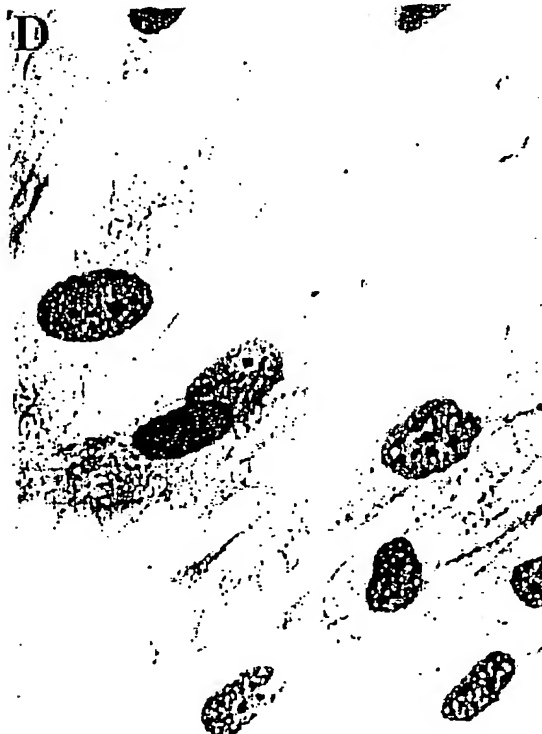


FIG. 24D (1)

LOCUS AF157612 5258 bp DNA INV 10-NOV-1999
DEFINITION *Toxoplasma gondii* acetyl-CoA carboxylase 1 (ACC1) gene, partial
cds.
ACCESSION AF157612
VERSION AF157612.1 GI:6164685
KEYWORDS
SOURCE *Toxoplasma gondii*.
ORGANISM *Toxoplasma gondii*
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; *Toxoplasma*.
REFERENCE 1 (bases 1 to 5258)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Growth of *Toxoplasma gondii* is inhibited by
aryloxyphenoxypropionate herbicides targeting acetyl-CoA
carboxylase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)
REFERENCE 2 (bases 1 to 5258)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
FEATURES Location/Qualifiers
source 1..5258
/organism="Toxoplasma gondii"
/strain="RH (EP)"
/db_xref="taxon:5811"
mRNA join(<1..90,547..702,2442..2672,3066..3421,4267..4582,
4941..>5258)
/gene="ACC1"
/product="acetyl-CoA carboxylase 1"
gene <1..>5258
/gene="ACC1"
CDS join(<1..90,547..702,2442..2672,3066..3421,4267..4582,
4941..>5258)
/gene="ACC1"
/codon_start=1
/product="acetyl-CoA carboxylase 1"

— FROM FIG. 24D (1) —
 FIG. 24D (2)

/protein_id="AAF04493.1"

/db_xref="GI:6164686"

/translation="RVLIANNGMAATKSIFSMRQWAYMELGDDK
 LLEFVVMATPEDMRANPEFIRRADKIVEVPGGPNRNNYAN
 VDLICQIAVQEKVDAVWPQWGHASENPNLPRRLSELGITFI
 GPSATVMAALGDKIAANILAQTAGVPSIPWSGDSLKATLDS
 TGAIPRDIFDQATVKSVEECEKVADRIGYPMMIKASEGGGG
 KGIRMVDRKEQVRGAYEQVVAEVPGPSVFMMLCTAARH
 IEVQIVGDEDGQAVALSGRDCSTQRRFQKIFEEAPPTTVVPP
 HTMKEMEKAAQRLTQSLGYVGAGTVEYLYNRKDDKFFFL
 ELNPRLQVEHPVSEGVGTGVNLPAACLQVAMGIPLWRIPDIR
 RFFGRDPNAGDRIDFINEDYLPIQRHVLASRVTAENPDEGFK
 PTSGRVDRLFQPLENVWGYFSVGASGGVHEYADSQFGHIF
 ATGKNREEARKKLVLGLKRVDVRGEIRTPIEYLVQLLEDKD
 FIENRIDTSWL"

BASE COUNT 1176 a 1271 c 1351 g 1460 t

ORIGIN

1 cgcgctctca tcgccancaa cggcatggca gccaccaagt cgatctctc catgcgctcag
 61 tgggcctaca tggaaactcg cgacgacaag gtgagcctga cacagtgaac aaggltggatc
 121 tcttgtagc ttcgaaatg ccatactctc aaaatgttga agagctgacc tgacgcaaaag
 181 ctaaataatc atgaagactc tctgtcacc gttagtggat tcccgtttg tcttgccccg
 241 ctctctatct tgttttcgc cgcaacagag aactgttaact gtatatacag tgatatatat
 301 agttatatgt acgtgttttt tatgcgcgta tgtgttcagt cacaactaca aaataaatgt
 361 acacgtacat gcttagatag ttacgtggcg acaaacctct tctgtgtcag ctatgcgaat
 421 cgcgcgaaaa ggcgaccgag acatgaagct ctctctcttc gcatttctag catttgcata
 481 cgcgtatgtg ggctgtgtgg aactgagtg gcagaggcat gtttgtgtat gtttttgtt
 541 gtgtagcttt tggagttcgt lgtgatggca acccagaag acatgcgagc gaactctgag
 601 ttcatctgcc gcgcagacaa gatcgtggaa gtccagggg gtccgaatcg caacaactac
 661 gcgaacgtcg atttaattg tcaaatcgt gtccaggaaa aggtgaggga gacgcaatgc
 721 ggggtgcgtc ctgctgtctg gtggacagtt taaagagcga attcattcag atggatagtg
 781 cgactcagaa gccctgaaag tctcgccttt atccagaggt cattaggtct acaggacctt
 841 ctgacgttca cactgagata ctacacgtct tctcagttg gaggttcttt gtttctct
 901 ttcatctct attcttcgcg ttttgcctc ttccctgtg ctagtcttc cgtgttcccc
 961 catttcaag tgcgtgtatg tctctctcat cactgcgtg gcgctgcgtt ttccgtcgtga
 1021 agggagaaga ctctctcttg ttctctctc cgtgtctcg gctctctcg actcttgccc
 1081 ttctttctg agaaggggaa agagttgggg aaccgagaa accggcgaga agacggcgca
 1141 tgagtgaagc cccggaaaac gggttccctg tcttcgggt gctctgtct tctctcttt
 1201 ctgcctattt cagcggatag aaaacgatct gcatagtccc tcttgaggtg gtccgtctt
 1261 aagctgtgga gttgtgcat gcagttccac agtgggcgtc ctctggagca gcagacctac

— FROM FIG. 24D(2) —

FIG. 24D(3)

1321 cctcactggg tctccattga tctgaacaaaa ctctatgcct ttccctctca ctcgcctctc
1381 ttccctctcg gcatcgcttt gccaggacct cctgtccctt caagaacac gcggcaggga
1441 ggcatctgat ggatcaclat gtcggctgat gatgtgtgg aagagctatt gcegcgttac
1501 tgtacaacct ctatcgtaaa ttttagagga gaaaacggat ctctctctgg aggtaccctc
1561 tctctgaaat ctatctgtc atccgattc tagggcgagg ttatgaagc acgcgcgcgt
1621 ctgtcgggtt gctctgatt ctgtttttg gcaagacgat ggaggatgaa cagaggaaat
1681 ttgtcact accactgacg agccgagagc tcatgattg gactgtccc tcatgaaat
1741 ctgacgcgtc gctttatag cgtttcgtc ctgaagcgt tctctctact ctctaggta
1801 ctctctcat ggcctctct ttgactgtc gggattccgt cactgttct gttgacttc
1861 gctactcacc ttctcccag tgtgcgtgt gtcgaaact cgtttgctt tactttctg
1921 tgtctctgga gacaaggatg aacagaggat tctattgta ctaccactga ggagcaacca
1981 gctcgtgat tggacttcc cctcattac atctagggt tctctctga aacattcgg
2041 ttctattct ctgttcgca tgcctcggg gtcctcggg acgtctctag cttaaccgc
2101 ttctccgce gccctgtgc ctgtttct ttgtcgtgt ttccctctc atggccgccc
2161 ttgattcat cgcgttctc ttccggatc ttctgtctc taattcaat caacatgagc
2221 tgttttcc tgtccgtct cctgtttg cgcgcgcata cccacgacga gcgcgaattg
2281 cgtcaagccc tccggtgtc cgtttcgcg agccgtgtc gttctgcctc ctctgcctc
2341 cctttaccg cgtctatct ttctgcgcg tcatctcgt ctgtctctg tctctctc
2401 ctgcatctt attccactc tgttttgcg tcttctta ggtggacgca gttgtggccc
2461 gattgggggca tgcacggag aatccgaat tgcctcgtc ttgtcggag ttggggatca
2521 cgttcattg ccttagtga acagtatgg ctgtctctg agataaact gcggccaaca
2581 tctcgcgca gacagcaggc gtccgagca ttccctggag tggagattc ctaaggcga
2641 cactcgacag caggggcgc attcctcgc atgtaagcag gcgtttac tatggacata
2701 atagacccct ttgagttc gactctcc gatgtatcc attcaggggc tctctctga
2761 ctctataagc agaaacgat gaacggacaa aaggaacgtg aagacctag acagggtaac
2821 atgcgcata atatatatat atattatat atacatatat ttatatatat atatatatat
2881 gtgaatgtc gaaaatgcca gtctccgca gtggtattt tgtggcaaca tgtatatca
2941 tataatgtg tgcatacaca tataataca tatatatata tatatatata tatatatata
3001 tataaataaa tatatgcaga ttgtgtatg tgcgtgcgga ctgcgtgtt tacgtttgt
3061 tttagattt cgaccaagcg acagttaaga gcgtggaggg atgcgagaag gtggcagacc
3121 gcattggta tccgatgat attaaagcga gtgaggagg cgggtgaaaa ggaattcga
3181 tggctgatc gaaggagcag gtccgcggg cgtacgagca agtcgtggc gaagtcaccg
3241 gatctctgt ctctatgat caactctga ctgccgcgc ccatatcga gttcagattg
3301 tgggggacga agatggacag gctgtcgtc tcatggccg cgtctcagc acgcaacgac
3361 gcttccaaaa gatatgtga gaagcaccgc cgacgactgt cgttctccc cacacaatga
3421 agtacgcaag agacacgac cggcaacaca aaatcctga acgcggaaag actgggagga
3481 cacagcccg aggagaagaa aaacaagaac gataaaggag ggggaaagcc aaggctaggg
3541 agaaaacgaa caaggataag ggaaggagga caacgaggag aaggggagga acagggcagt
3601 gaagacgaga gcacgaccgc tgaaccaag atcggctc gccctcgggt tcatggtgt
3661 gtgactct cgcgaggcgg gtcgagtga tttgtctg aggcgtctt cctgagggt

— FROM FIG. 24D (3) —

FIG. 24D (4)

3721 cagtgcctaga gagggacgga aaggatgaac gagttgacgt tcaccgttgc gcggagagtg
3781 aaaaaaaaaag actgctttgt ggggtgtcca ccttctca aacgtcgcgg cacatttta
3841 agccttccag tggccactct aaaccacgcg agggtaagc aggtgtgcaa cagagactg
3901 ttctgtcag tcttgcctc ttactcctt ctcttctccg agagagaaaa tggaacggag
3961 gcagtatccc gagatcgaca gaatggcttc gcatctgct tegtcttcc cctcacttta
4021 tcggaaagtg ctctgaaaga tccitgaagg cgagagaggg cggacggctc cgcgaactct
4081 acttgccttg cgtgattgt ctgccgtgag tgactctgg tctctgtgt ctctggctc
4141 ccgtttagcg gglttccct cgattcttc aagagagtta ctgtgggtt tctcccgaca
4201 tccgctggag acctggaagc gcgctcttcg tcttcacagc gtctttgac ttgtgtctg
4261 tcgcagagag atggagaaag cagctacgcg cctgacgcag tctctgggt acgtgggcgc
4321 cggcacctgc gagtactgt acaatcgaaa agacgacaag tttcttcc tcgagttgaa
4381 tccgagactg caggtggagc atcctgtctc ggagggcgtc accggtgtca atttgcgcgc
4441 tgtcagctc caagtggcca tgggaattcc tctgtggcg attcagata ttgcgcgtt
4501 ctgtggcgga gacccaaacg caggcgaccg catcgattc atcaatgagg actaccctcc
4561 catccagcgc catgtctctc cggtagcaa ctggatgcaa cgaacgcctg cgcattgagc
4621 ttctacgtg gtgtgtctc cgatactact aaaaagtgt catcgcgaca tgtcagttg
4681 tgtgacgtg agtcgcaatt gtaactgaaa agaagtcata aatattcaaa aactgttca
4741 atactgtcc acgtaccgat acacacatac acatactaa tatatatata tatatcgtg
4801 catacgtact tcaaatacat acatacatac atacatcgat acacatgata tatatatata
4861 tagatatata tggtttttg ttccctttg ttgagcgggt ggaagtgac ggattgatt
4921 ggaagttct ttgtttcag tctcgagtga cggcggagaa tcccagcga ggattcaagc
4981 cgacgagtg tcgcgtagat cgcctggat tccagcctc ggagaacgtc tggggatact
5041 ttccgtggg cgcagtgga ggggtccacg agtacgcaga ttctcagtt gggcacatt
5101 tcgcgacggg gaagaatcgc gaggagggc ggaagaagct ggtgtcggc ctgaagcgcg
5161 tggatgtccg tggcgagat cggacgcaa tcgagtact ggtgcagct ctggaagata
5221 aagactcat cgaaaaccgc atcgacacat cgtggctc

— FROM FIG. 24D(4) —
FIG. 24D(5)

LOCUS AF157613 6965 bp DNA INV 10-NOV-1999
DEFINITION *Toxoplasma gondii* acetyl-CoA carboxylase 2 (ACC2) gene, partial
cds.
ACCESSION AF157613
VERSION AF157613.1 GI:6164687
KEYWORDS
SOURCE *Toxoplasma gondii*.
ORGANISM *Toxoplasma gondii*
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; *Toxoplasma*.
REFERENCE 1 (bases 1 to 6965)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Growth of *Toxoplasma gondii* is inhibited by
aryloxyphenoxypionate herbicides targeting acetyl-CoA
carboxylase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)
REFERENCE 2 (bases 1 to 6965)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
FEATURES Location/Qualifiers
source 1..6965
/organism="*Toxoplasma gondii*"
/strain="RH (EP)"
/db_xref="taxon:5811"
mRNA join(<1..39,412..600,902..1222,2554..2783,3357..3531,
3981..4130,4687..4812,5274..5360,5770..5826,6311..6426,
6938..>6965)
/gene="ACC2"
/product="acetyl-CoA carboxylase 2"
gene <1..>6965
/gene="ACC2"
CDS join(<1..39,412..600,902..1222,2554..2783,3357..3531,
3981..4130,4687..4812,5274..5360,5770..5826,6311..6426,
6938..>6965)
/gene="ACC2"
/codon_start=1
/product="acetyl-CoA carboxylase 2"
/protein_id="AAF04494.1"

— FROM FIG. 24D(5) —

FIG. 24D(6)

/db_xref="GI:6164688"

/translation="RILIANNGTAAVRCIRSMRHWAYEALGNSKALEFVVMATAA
DIDANAEFIAEADFYVEVPPGPSNNYANLHLIVQTAETYECD
AVWPGWGHASENHRLPAILQTLKRKTIWIGPSPQAMLALGDK
IGSAVIAQSVNVPCVPWSGETRSPKRADTQPHSKTRRSISPPHFH
TRESMHLSISVSKVFLTCLWTHFAFPLHQVLDCCAKIGYPVMIK
ASEGGGGKGIRRVTNAAEEVADAYRQVVNEVKGSPVFVMRMVS
DCRHLEVQLLADKSGRCVSLGSRDCSIQRRRCQKIIIEGPVVAAP
PEVVSQMEDAACRMAMAVGYENAGTCEFLYDPKTHQFAFLEV
NARLQVEHVVTCEVGDENLPAAQLQVAMGILIDDIPDIKAYLD
SAASNKPVGKHIIAARITAEHAEESFRPTVGLVHELTFRPSRFVW
CYFSIGSKGNIHAFNDAQFGHLFAHGKDRREAVKHMVLALKD
MTIRGELRTNVEALIKILEHPDFVANETHTTWL"

BASE COUNT 1683 a 1627 c 1841 g 1814 t

ORIGIN

1 cgcacccca ttgccacaa cgggactgcc gctgttaggg tgagtgtgt ttctcatgc
61 agcgtgtgag tacagagccg cgagctttt ttctgccaa ctctctctcc aaattccctg
121 aagtcaggga agtagagcgc cggcacgccc ggggcgcggg gaaaggggga gaaagcggcg
181 agagaaacgg gggcggaagc ggggagccac aagcacagga ctctgcgaaa aaaacggagc
241 tctgcaggca aggcgggaga ggaacaagaa gggaggaaag cgaagggtga agggcggggc
301 aagaattatg acaaggggac gagaagctgg agggagatct gcagcgcgaa gctgtcgaaa
361 acgcaatcat gttgccgacc ctggagttc acctctccgc gcttctgca gtgcattcga
421 agcatgcgtc actgggcgta tgaggcgctc gggaacagca aggccctcga attgtcgtg
481 atggccactg cagcggacat cgacgccaac gctgaattta ttctgaagc agactctac
541 gtggaagtc ctcctgggac gaactcgaa aactacgcca atctgcattt cattgtacag
601 gtaaaagtta cggaacaggc caaccgaacg ccggaggaaag cgcgacagcg gcgtcgttt
661 ccatacgccg agagcgttc ctctcacag cctgttctgc atttcggcg ttgcagacag
721 aggaccgcgc agaacgcggt ggcacgaacc cagtttcacc gcacaacggg agccgtcgtc
781 agtagcggac gaactctagc gtctgtgcgc agtcaatgtg aggcattcgg acgtgaggac
841 gctctgtgcg ggtgcgactg gtctgaagcc ggcgatgcgt tgattttct tctttcgca
901 gacagccgag acgtacgagt gcgacgccgt gtggccagge tgggggcatg cgtcggaaaa
961 tcaccgccta cctgcgatt ttgcagacgt gaagaggaaa acaatttga ttggaccag
1021 cccgcaagcg atgtctgcgc tggcgacaa gatcggaat gcccctcag ctacgtccgt
1081 caacgtgcc tttgtgccct ggtaggtga gaccagaagc cccaagcgcg cagacacaca
1141 gccgcacagc aaacacggc gatcgatct tccacccac ttccacacac gagaatctat
1201 gcatttgtct atatttgtat ctgtatata atatatata acgtatatgt atatatata
1261 atatatata gcatgttaa atgggtacgc cgttcagag ccgtggccac agaaagacag
1321 gcatttgtgg agttgtccg atgaactatg caaacaagtc gtgaactgg cttttctc
1381 ccgttttga catctttac gacttttga cgtgtgacgc atcaagaac acacacacac

— FROM FIG. 24D(6) —

FIG. 24D(7)

1441 tcaaaatata tglaaatag tatatgtatg catttgiacg tatatatata tatatatata
1501 tatatatata tatatatata ttgcttgtat tatatatgtat tatgtttgag agtggtagga
1561 ccttcattgtg tatgtatata gcggggactg ctagtgtgtt ttgtgtgtgt catgtgcgag
1621 ttccttgcg acgaaaactg cagtattctt cagttatcca gtccttgcg aatttgaatt
1681 gaaacacggc agctaaatca acaggggtcg catgcatgtt cccgtgagga aagggtgact
1741 tagtcggctg ttcccttgtg caatgatgcg caagtcgalt caacagagtc caacgtctac
1801 gatcgtggat tcagagtcca ggactacgtg acgttcagga acgcggccgt ctgcagctt
1861 tgaagaaac gtgtcaaac gtgctgtatg caaacctctg gtaaacgac gtgtgaaagt
1921 tctctttcc gtactctgt tgcctttcc ctacattgt tgcgtttct gtgttgact
1981 tgccttctt gcatctctt ctgttttta tgtttcagg catggacgtc actgtggacc
2041 tgagtcgaagt cgacccacc aaaggccgtt cgcagcagac actgcagctt gcatgcgtg
2101 agtcggccaa ggatgtaggc catgccaaa gtttttcc caggaaaagt ggatttgc
2161 cggaatgca agtgaatata cgagagagcg ctccggccca taggtcgcca tccgttctc
2221 cgtcaacca ctgtttcac ttctcttag gcgtatgtg gtctctatat acgcattat
2281 ctatcaatcg tgtctatgt ctgggacgcc gccggctgt ctagaacggc aatgtatga
2341 catacgcaag atgcctctga aggcggccaa ggacgtgcag tcaattctgt ctacagaccg
2401 agattcatag atgcagatcc ccacagagat acacctgcgc atgccaaagc acacacgc
2461 atctatatat aaaaatacat atagagaggg ctctctagac tcacatatat atatatatat
2521 atgtaaatgc atataaatag atgcgcattgt tagaaggctt ttgtacgtg cctgtggac
2581 catttgcct tccgttaca tcaggctctg gactgttgcg cgaaaattgg atatccctg
2641 atgattaagg cgagtgaagg agggggcgcc aaaggcattc gtgcagtcac gaacgcagag
2701 gaggtcgccg acgcgtatcg ccagggtgtc aacgaagtc aaggctctcc agtgttgc
2761 atgcgcattg tctccgattg caggctcgtt atttctctt ttgtcgtgc tccacctct
2821 cgcgtattg tctttccat tgccttagct gtctccgtt tgcctcatt cctctctct
2881 cgtcgcgtc tctggctca tgcgcgtgt cgcacgtcg cctctgtcaa gacgcaggt
2941 ttacatcca cctgcgcgc gacgagcgcc gcgaaactct tgaagagctg agcggctgtc
3001 tggttgagag aaaatacat ttgcgtctc cgcgaggctt ccaggctacc aggggtcggg
3061 tcgaacgaag aggttccacg tggaaaacga gtcccgtcga ctggtggcgg tctgttct
3121 tgcgcgggg gcttcgcgtt tgcgggggtg gctgcttct tggaaactcg tgcctagtcg
3181 tglgaagtga acacgaacgc gtttccatcg acctgggaaa caggcggaaa cgcgaatgt
3241 gagatccgt cgaagggtgt aacagacagc atttccagcg aagaagctga gaagcagacc
3301 ttctcagtt ccggtccat cgtgtcagc ccttccact tgcgcgtgt gtacagacac
3361 ctggaggctc agctcttggc agacaagtc gggcgggtcg ttctgcctgg aagtcgggac
3421 tgcctaattc agagaagatg ccaaaaaac attgaagaag gccctgtct tgcagctct
3481 cccgaggtcg ttctcaaat ggaggacgtt gctgcggga tggctatggc ggtgagtgtg
3541 agcaaataga gccctacgca agttgccgtg agaaaactga atctccatgg gatgccatt
3601 tgaagctca caggaaacgc taaagctaca tgccttga cgtttccct cggacgcca
3661 gtacacaag agtaccctt tactccgaga tgaccgctt acatagaagc atatagtcgt
3721 atattcagat acgcctgat gcttgggtat gtccagtgc acctacgtat atacacagac

— FROM FIG. 24D(7) —

FIG. 24D(8)

3781 ggtatitgc atgegacttt atagttcaaa tgtgtacaca tccattaaaa tatacatata
3841 tgtatatata tgtatattta tataratgcg ratgcatgta taccitcgta gacgtgtgtg
3901 tgtgtgtgta catgtgtggc cagcgggtata cacttacaca tgcattgcatt gattgggttt
3961 ctgttttatt ttgtttgcag gtgggggtatg agaattgcggg aacatgtgag ttittgtacg
4021 accccaaaaac taccagttt gcgtttttgg aggtgaacgc gcgcctccaa gttaggcacg
4081 tcttcacaga gtgcgtcggg gacttcaacc tcccggcggc gcagcttcag gtatagctt
4141 acgcagcctt cttaaaaag gcgaaaagaa cgtctcgtt tgccttgtt taccggccc
4201 acggcctcgt tgacacagac tcatitgaac acaaatataa acgatacaca attccatata
4261 tatatatat atatatatat atatatatat atatatatat atatatatat
4321 ctgtatgtag tataggata tatgaagata accacaaagt acctctatgt atggatacat
4381 acgttcatgc gttatcttt gttatgtgc atgcgagagt gtatcgtgcg tctgtgtgtg
4441 taggctaggt gcaactgtca gtagggtgat gcatgatc taaatatata gatttacata
4501 cttttgctg cctgtcttc tctgccaca cttataacc acatatatat atatatatat
4561 atatatatat atatatatat atgaatatgc gtgattttc tggcgttgt gcatgcgtca
4621 tccgttgatt tggagggacg gggaaagcga tgcgcgcgt ttctctgt tgcctttct
4681 tccaggttg cgttggggat cctgatgat gacatccag atatcaaggc ctacttggac
4741 tggcgggcca gcaacaagcc cgttggaaaa cacatcatg cagctcggat aacggcggag
4801 catgcagaag aagttagctg ttgttccca cgcactcagc ggagtcgtt ttctgtctt
4861 tctttacctt cgtcgcgaat cctacatggg caaaacgtcc gcatacccc cttctgtgt
4921 gtgtgtgtat cttagcttt tcatgttct cgttcctgc gtatcgggtt aactgtacg
4981 cgttgcatt ccatcatca acgtcgtgc ttccacctt tctttctt tctctgtt
5041 cgtgtctgcg tctctactt acgttgtgt acctttcca ttctgttat cgtgtctg
5101 gtggatctc gtttatcgc gtgcgagag agaggagtgc ggtaaacgag tgacaaacac
5161 gggaggttg ttgtcacc cgtgaatgtt cttcgcgtt tctgaacgag gcgcgggaatg
5221 cgtctttgc actgcattca actttctt tctcgggtca tgcgcgcatt cagttctt
5281 gaccgacgt cggcctcgt cagagctca cgttgcgcc gtgcgcctt gtgtgggggt
5341 attttcat cggcagcaag gtgaggaagc cgggaagatt ctgagttt cgcacaggt
5401 ttgggaacc ggaaaactgc gagaagaca gcgagacgt gtccgaggg aattcttgc
5461 tggctccaaa gcgtcagcg ctatctcag tggatggaaa cctcatcca gacttaaac
5521 cagagacgc accagacga gtctctgt ttctcgtt ctctgtgtc tgaattac
5581 tgccttct gaacgcgagt cgtcggct acctctct gtccctgcc acttgagag
5641 aggtgaacaa gtgcgttg cgtccagag ggtctcgt cctgtgcct tactctct
5701 ctggtgtctg ggcaactgc ggtctgtca aaaagcttg ctctccgac gtctgcct
5761 cctcacagg gaaacatcca cgcgttaac gacgtcagt tccgacat ctctgcacac
5821 gggaaggtag gaaggaaggc aagaacgagg acagagaacg ctccgagaga gagagcgaaa
5881 cggagacaga gaaagagct ccaaggcaga caccagatg gccgcagga acgagagaca
5941 gacgaagagg aagggagggg caacagggga agaccaagg agggagagag gcgcaatgca
6001 agagtacga gggagagaag gagagaaacg caggagggga cgcagtgtc aggaagaaaa
6061 acattgcgt ctggggtat cagagaagag agtgaccga tgcattgctg tctgggtgc

FIG. 24D (9) FROM FIG. 24D(8)

6121 cgatcttggc tgaatatgag tgactgcaca cgaagagaga agagaagaga aaagaggaaa
 6181 aaataaatgt ggacgtgtga atgacctga agacaggggg acgaaaattc tcttggcgga
 6241 cgtgagagcg aggcctgaaa aagcgaccaa gagactcgcg acttgacgtt tggcattgt
 6301 tcaattgcag gacagacgag aagctgtcaa acacatgggt ctggcgctca aggacatgac
 6361 aatccgaggg gaactgagaa cgaatgtaga ggctctgac aagattctgg aacatctga
 6421 ctctgttaa gcatcttcg tgcacttag ccttagacc acaaatcac cagcgctctg
 6481 tgcatacag aactcacat cacagtcac atggaaatcc cgcgcctga tatatatata
 6541 tatatgaaa tatatgaaa tatatgata tatatatata tattgtatg tatggcagca
 6601 cactgtctct gtaatgtat ttgtaagtc attgcatct cggcgctccg gtcctcagtc
 6661 gtgggtatcc gtgtaaagt ccttatagc acgtgagtg tgcctgtgt ccgtgaatc
 6721 tgtattctt cgtggagatc tgtgtgtgt gacagctgag tgtgggtga acccgagaa
 6781 gcgccttct gcgagttgt attactaag actcctctt gctctgttag aacagcgatg
 6841 tattgtctga ggcgcgggt gagaatgat gtcgaaacc atcccggtaa aagggtgacg
 6901 cctgcgtgca ttagtgaat atgttctt tctccagag caatgaaacg cacacgacat
 6961 ggctg

FIG. 24D (10) — FROM FIG. 24D (9) —

LOCUS AF157614 393 bp DNA INV 10-NOV-1999
DEFINITION *Cryptosporidium parvum* acetyl-CoA carboxylase 2 (ACC2) gene,
partial cds.

ACCESSION AF157614

VERSION AF157614.1 GI:6164689

KEYWORDS

SOURCE *Cryptosporidium parvum*.

ORGANISM *Cryptosporidium parvum*

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Cryptosporidiidae; *Cryptosporidium*.

REFERENCE 1 (bases 1 to 393)

AUTHORS Zuther, E., Johnson, J.J., Haselkorn, R., McLeod, R. and Gornicki, P.

TITLE Growth of *Toxoplasma gondii* is inhibited by
aryloxyphenoxypionate herbicides targeting acetyl-CoA
carboxylase

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)

REFERENCE 2 (bases 1 to 393)

AUTHORS Zuther, E., Johnson, J.J., Haselkorn, R., McLeod, R. and Gornicki, P.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA

FEATURES Location/Qualifiers

source 1..393

/organism="Cryptosporidium parvum"
/db_xref="taxon:5807"

mRNA <1..>393

/gene="ACC2"
/product="acetyl-CoA carboxylase 2"

gene <1..>393

/gene="ACC2"

CDS <1..>393

/gene="ACC2"
/codon_start=1
/product="acetyl-CoA carboxylase 2"
/protein_id="AAF04495.1"
/db_xref="GI:6164690"
/translation="SSGGGGKGIKRLCSSMEDLESNYRQVINEVKGSQ
VFVMRAVVKCRHLEVQVLGDYGDVFALSTRDCTIQRRHQ

FIG. 24D (11) — FROM FIG. 24D (10) —

KVIEEGPVTIVSQEIVKELELSAERMCKAVGYSSAGTVEFLY
DIERSCIAFLEVNARL"

BASE COUNT 129 a 54 c 104 g 106 t

ORIGIN

1 agctcaggag gtggagggaa aggtatccga ctctgcagtt ccatggaaga cctagaatca
61 aattacagac aagttataaa tgaagttaaa ggtagcāaag ratttggtat gcgagcagtt
121 aataagtgtg ggcacctaga ggttcaagta ctāggagaca aatatggtga cgtgttccga
181 ttgagcacia gagattgcac aatacagagg cgtcaccana aggttataga ggaaggggcca
241 gtacaattg tgagicaaga gattgtaag gaattggagt tatctgcaga gaggatgtgc
301 aaagctgtgg gttattcatt tgcaggaact gttagaattc tatatgatat tgaacgttca
361 tgtatagctt ttctagaagt taatgccaga tta

TO FIG. 24D (12)

FIG. 24D (12) — FROM FIG. 24D (11) —

LOCUS AF157615 393 bp DNA INV 10-NOV-1999
DEFINITION Plasmodium falciparum acetyl-CoA carboxylase 1 (ACCI) gene,
partial cds.

ACCESSION AF157615

VERSION AF157615.1 GI:6164691

KEYWORDS

SOURCE malaria parasite P. falciparum.

ORGANISM Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 393)

AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.

TITLE Growth of Toxoplasma gondii is inhibited by
aryloxyphenoxypionate herbicides targeting acetyl-CoA
carboxylase

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)

REFERENCE 2 (bases 1 to 393)

AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA

FEATURES Location/Qualifiers

source 1..393

/organism="Plasmodium falciparum"

/strain="FVO"

/db_xref="taxon:5833"

/country="Viet Nam"

/note="not cloned; isolated from US soldier evacuated from
Vietnam to Fort Ord; supplied by J. Barnwell"

mRNA <1..>393

/gene="ACCI"

/product="acetyl-CoA carboxylase 1"

gene <1..>393

/gene="ACCI"

CDS <1..>393

/gene="ACCI"

/codon_start=1

/product="acetyl-CoA carboxylase 1"

/protein_id="AAF04496.1"

FROM FIG. 24D (12)

FIG. 24D (13)

/db_xref="GI:6164692"

/translation="SQGGGGKGIRKVENEYEIKKAYEQVQNELPNS
PIFLMKVCNNVRHIEIQVVGDMYGNVCSLSGRDCTTQRRFQ
KIFEEGPPSVVPYPIFREMEKSSIRLTKMIKYRGAGTIEYLYD
QINKKYFFLELNPRL"

BASE COUNT 156 a 39 c 72 g 126 t

ORIGIN

1 tcacaagggtg gtggtgggaa aggtatcga aaagtggaaga atgaatatga aataaaaaaa
61 gcatatgaac aagtacaaaa tgaattacct aattctecta tattttgat gaagggtgt
121 aataatgtaa gacatatga aatacaagtt gttggtgata tgtatggaaa tigtgttct
181 ttaagtggtc gtgattgtac tacacaaaga agatttcaaa aaatttttga agaaggacca
241 ccategttg taccatalcc tatattcga gaaatggaaa aatcatctat acgattacct
301 aaaatgatta aatatagagg tcttggaact attgaatatt tgtatgatca aataaataaa
361 aaatatatt tcttagaatt aaatccaaga tta

— FROM FIG. 24D (13) —

FIG. 24D (14)

LOCUS AF157616 393 bp DNA INV 10-NOV-1999
DEFINITION Plasmodium knowlesi acetyl-CoA carboxylase 1 (ACCI) gene,
partial cds.
ACCESSION AF157616
VERSION AF157616.1 GI:6164693
KEYWORDS
SOURCE Plasmodium knowlesi.
ORGANISM Plasmodium knowlesi
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 393)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Growth of Toxoplasma gondii is inhibited by
aryloxyphenoxypropionate herbicides targeting acetyl-CoA
carboxylase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13387-13392 (1999)
REFERENCE 2 (bases 1 to 393)
AUTHORS Zuther,E., Johnson,J.J., Haselkorn,R., McLeod,R. and Gornicki,P.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Molecular Genetics and Cell Biology,
University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
FEATURES Location/Qualifiers
source 1..393
/organism="Plasmodium knowlesi"
/strain="H"
/db_xref="taxon:5850"
/country="Malaysia"
/note="supplied by J. Barnwell"
mRNA <1..>393
/gene="ACCI"
/product="acetyl-CoA carboxylase 1"
gene <1..>393
/gene="ACCI"
CDS <1..>393
/gene="ACCI"
/codon_start=1
/product="acetyl-CoA carboxylase 1"
/protein_id="AAF04497.1"
/db_xref="GI:6164694"

— FROM FIG. 24D(14) —

FIG. 24D(15)

/translation="SQGGGGKGIRKVENEEI KKA Y TQVQMELPNSPIFLMKVC
SNVRHIEIQVVGDMYGNVCSLSGRDCTTQRRFQKIFEEGPP
SVVPPNIFREMEKASIRLTKMIKYRGAGTIEYLYDQEKQTY
FFLELNPRL"

BASE COUNT 138 a 69 c 91 g 95 t

ORIGIN

1 tcacaaggag gaggggggaa aggtatcgg aaagtggaga acgaagaaga aataaagaaa
61 gcctacacac aagtgc aaat ggaattaccc aactcgcta tctttcta at gaaagtctgt
121 agcaacgta gacacatcga aatacaagtt gtggggata tgtatggtaa tgtatgctcc
181 cttagtggaa gagactgcac gacccaaagg aggttccaaa aaattttga agaagggtcc
241 ccttcagttg tacctccgaa tatttccgt gaaatggaaa aggcacccat acgtctaaca
301 aaaatgataa aatatagagg tgcgggaact attgagtatt tatatgacca ggagaagcag
361 acttattttt ttctcgaatt aaatccctga ctg

FIG. 24E

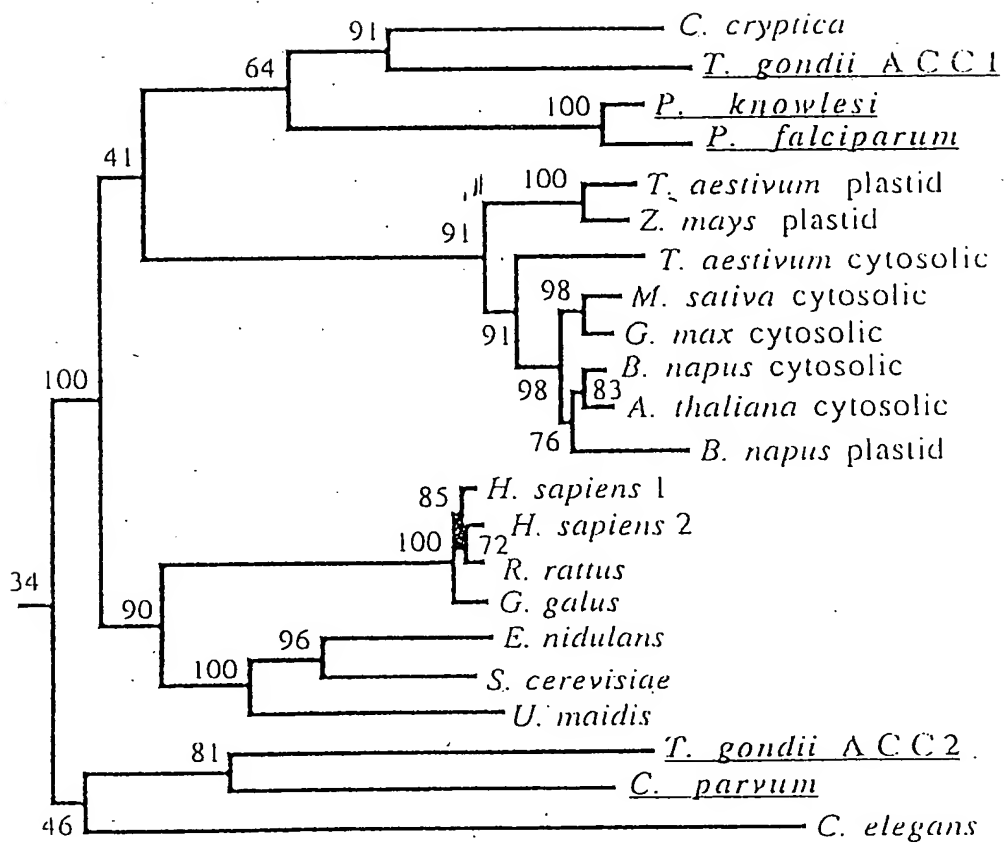


FIG. 24F

Aryloxyphenoxypropionates (fops)

Haloxypop: $X=CF_3$, $Y=Cl$

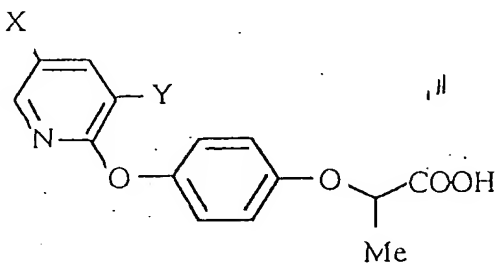
Haloxypop methyl ester

Haloxypop ethyl ester

Fluazifop: $X=CF_3$, $Y=H$

Clodinafop: $X=Cl$, $Y=F$

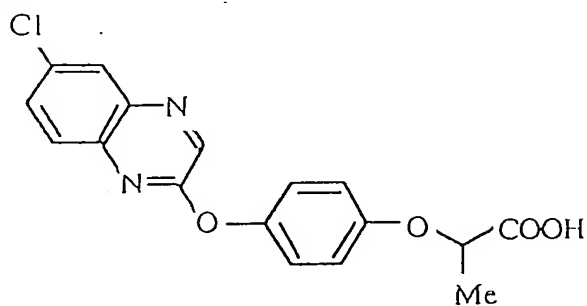
Topik, clodinafop propargyl ester



Quizalofop

Targa, quizalofop ethyl ester

Agil, quizalofop 2-isopropylideneaminoxyethyl ester



Cyclohexanediones (dims)

Sethoxydim: $X=CH_2CH(CH_3)SCH_2CH_3$, $Y=CH_2CH_2CH_3$, $R=CH_2CH_3$

Cethoxydim: $X=C(SCH_3)CH_2$, $Y=CH_2CH_3$, $R=CH_2CH=CH_2Cl$

Clethodim: $X=CH_2CH(CH_3)SCH_2CH_3$, $Y=CH_2CH_3$, $R=CH_2CH=CHCl$

